

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 27, 1999, 18:22:40 ; Search time 556.3 Seconds
(without alignments)
12036.795 Million cell updates/sec

Title: US-08-699-716A-1

Perfect score: 1566
Sequence: 1 ATGGGCATCATCATCATCA.....ATGACACGCTCGTAATGA 1566

Scoring table: IDENTITY_NUC

Searched: 780561 seqs, 2137953050 residues

Database :

GenEmbl:*
1: gb_bal:*
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40: gb_bal:*
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43: gb_bal:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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BEST AVAILABLE COPY

1	1473.6	94.1	1530	5	A56814	A56814 Sequence 22
2	1410.6	90.1	1462	5	A56808	A56808 Sequence 16
3	979.4	62.5	2100	1	YEPICR	M26405 Yersinia pe
4	979.4	62.5	70305	1	YPCD1	Al117189 Yersinia
5	979.4	62.5	70504	2	AF053946	AF053946 Yersinia
6	979.4	62.5	70559	2	AF074612	AF074612 Yersinia
7	976.8	62.4	1014	5	A46411	A46411 Sequence 1
8	976.8	62.4	1014	5	A56793	A56793 Sequence 1
9	974.8	62.2	1014	5	A46413	A46413 Sequence 3
10	974.8	62.2	1014	5	A56795	A56795 Sequence 3
11	957	61.1	981	1	YEPICR	X96802 Y.pseudotub
12	953.8	60.9	2201	1	YEPICR	M57893 Yersinia ps
13	927.4	59.2	63673	2	AF102990	AF102990 Yersinia
14	916.2	58.5	975	1	YEPICR	X96801 Y.entocol
15	914.6	58.4	975	1	YEPICR	X96797 Y.entocol
16	913	58.3	975	1	YEPICR	X61996 Y.pstis ge
17	911.4	58.2	975	1	YEPICR	Al117211 Yersinia
18	890.4	56.9	1002	1	YEPICR	AF053947 Yersinia
19	882.4	56.3	1002	1	YEPICR	AF074611 Yersinia
20	516.8	33.0	5383	1	YPCAF	A56812 Sequence 20
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23	516.8	33.0	100990	2	AF074611	AF010149 Pseudomon
24	516.8	33.0	547	5	A56812	AR000030 Sequence
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26	74	4.8	4168	2	AF010149	AJ011856 Saccharom
27	74	4.7	660	14	AF081364	I66494 Sequence 14
28	53.4	3.4	1402	5	AR000030	AC005139 Plasmodu
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30	48.2	3.1	85779	7	SCE011856	AC005140 Plasmodu
31	48	3.1	7218	5	I66494	AL049181 Plasmodu
32	47.8	3.1	256172	34	AC005139	AL034557 Plasmodu
33	47.8	3.1	155573	34	AC007926	AF044866 Phoebs s
34	47.8	3.1	110000	42	AC005140	AL010773 Plasmodu
35	46.8	3.0	293431	33	PFMAL13P4	AL035477 Plasmodu
36	46.8	3.0	110000	33	PFMAL13P4	M59744 D. discoidu
37	46.4	3.0	1158	35	AF044866	AE001426 Plasmodu
38	45.4	2.9	314303	42	AC006279	AL035476 Plasmodu
39	45.2	2.9	21202	21	PFSC04088	AC005308 Plasmodu
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45	44.2	2.8	190112	43	AC011454	

ALIGNMENTS

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LOCUS	A56814					
DEFINITION	Sequence 22 from Patent WO9628551.					
ACCESSION	A56814					
NID	93712827					
VERSION	A56814.1	GI:3712827				
KEYWORDS						
SOURCE						
ORGANISM	Yersinia pestis.					
REFERENCE	1 (bases 1 to 1530)					
AUTHORS	Titball,R.W., Williamson,E.D., Leary, Sophie,E.C., Oyston,P.C.,					
TITLE	VACCINES FOR PLAGUE					
JOURNAL	Patent: WO 9628551-A 22 19-SEP-1996;					
COMMENT	SECR DEFENCE (GB)					
FEATURES	Other publication ZA 9602036 960716					
	Location/Qualifiers					
	1..1530					
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TITLE VACCINES FOR PLAGUE
JOURNAL Patent: WO 9628551-A 16 19-SEP-1996;
SECR DEFENCE (GB)
COMMENT Other publication ZA 9602036 960716
Other publication AU 4951196 961002.
FEATURES Location/Qualifiers
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QNPQHFIEDLEKRVBOLTHGSSVLELVOLVKNKIDISIDYDRKQSEVFNANVI
TDDIELLKILAFLEPEDAILKGGHNDONQNGIKRYKEFLLESSPNTOMELRAFMAVM
HSELTADRIDDLIKVIVDSMNHGARSRLRELEIAETLEKITSYIOAEIKHHS
SCINIHDKSINIMDKNLVYCTDEIFKSAEKKILEKMQTTIYVDGSEKTVISIKD
FLGSENRKGTALGNLKNYSYKNDNLSLHFAITTCSDKSRPLNDLVSKTQLSDITS
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BASE COUNT 476 a 286 c 300 g 400 t
ORIGIN

Query Match 90.18; Score 1410.6; DB 5; Length 1462;
Best Local Similarity 99.18; Pred. No. 3e-298;
Matches 1432; Conservative 0; Mismatches 4; Indels 9; Gaps 1;

QY 131 CGGCAGATTAACTGCAAGCACCAGCACTGCTGTGAACCCAGCCGCAATCA 190
DB 6 CGGCAGATTAACTGCAAGCACCAGCACTGCTGTGAACCCAGCCGCAATCA 65
QY 191 CTCTTACATATAGGAAGGCGCTCCATTTACATTTATGACAAATGAAACATGATACAG 250
DB 66 CTCTTACATATAGGAAGGCGCTCCATTTACATTTATGACAAATGAAACATGATACAG 125
QY 251 AATTACTGTTGGTACGCTTACTCTTGGCGGCTATTAACACGAAACCACTAGCAATCTG 310
DB 126 AATTACTGTTGGTACGCTTACTCTTGGCGGCTATTAACACGAAACCACTAGCAATCTG 185
QY 311 TTAACTTTACAGATGCCGCGGGTATCCCATGCTTAACTTAACTTCTAGATGAA 370
DB 186 TTAACTTTACAGATGCCGCGGGTATCCCATGCTTAACTTAACTTCTAGATGAA 245
QY 371 ATAACCAACAATTCACATACAAAAGTATGGCAAGATTCAGAGATTTGATATCTCTC 430
DB 246 ATAACCAACAATTCACATACAAAAGTATGGCAAGATTCAGAGATTTGATATCTCTC 305
QY 431 CTAAGGTAACGATGAGAACCTTGTGGGGATGACGTCCTTGGCTACGGGACGAGG 490
DB 306 CTAAGGTAACGATGAGAACCTTGTGGGGATGACGTCCTTGGCTACGGGACGAGG 365
QY 491 ATTCTTTGTTGCTCAATGTTGTTCCAAAGCGGTAAACTTGCAGCAGTAAATACACTG 550
DB 366 ATTCTTTGTTGCTCAATGTTGTTCCAAAGCGGTAAACTTGCAGCAGTAAATACACTG 425
QY 551 ATGCTGTACCGTAAACGATCTAACCAAGAAATCAT-----GATTAGAGCTACG 601
DB 426 ATGCTGTACCGTAAACGATCTAACCAAGAAATCATGGAAGTCGTTATGAGCTACG 485
QY 602 AACCAAAACCAACATTTTATGAGATCTAGAAAAAGTTAGGGTGGAGAACACTACTG 661
DB 486 AACCAAAACCAACATTTTATGAGATCTAGAAAAAGTTAGGGTGGAGAACACTACTG 545
QY 662 GTCATGTTCTTCAGTTTATGAGAAATTTGTTGCTGATTAGTAAAGATTAATAATATAGATA 721
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DB 666 ATGATATCGAATTTGCTCAAGAAAAATCTTACTTATTTTTCACCCGAGGATACCATTTCTTA 725
QY 842 AAGCGGCTCATTTATGACAAACCACTGCAAAATGGCATCAAGCGAGTAAAGAGTCTCTG 901
DB 726 AAGCGGCTCATTTATGACAAACCACTGCAAAATGGCATCAAGCGAGTAAAGAGTCTCTG 785
QY 902 AATCATGCCGAATACACAATGGGAATTCGGGCGTTTCATGCGAGTAATGATTTCTCTT 961
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DB 846 TAACCGCGCATCGTATGATGATGATATTTTGAAGATGATTTGATTCAATGATATC 905
QY 1022 ATGGTATGCCCGTAGCAAGTTGGTGAAGAATTAGCTGAGCTTACCGCGGAATTAAGA 1081
DB 906 ATGGTATGCCCGTAGCAAGTTGGTGAAGAATTAGCTGAGCTTACCGCGGAATTAAGA 965
QY 1082 TTTATTCAGTTTATTCAGCCGAATTTATTAAGCATCTGCTAGTAGTGGCACAATAATA 1141
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QY 1142 TCCATGATTAATCCATTAATCTCATGATGATTAATAATTTATATGTTATACAGATGAAGA 1201
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QY 1202 TTTTAAAGCCAGCGGAGTACAAAATCTCGAGAAAATGCCCAACCACTTACAG 1261
DB 1086 TTTTAAAGCCAGCGGAGTACAAAATCTCGAGAAAATGCCCAACCACTTACAG 1145
QY 1262 TGGATGGGAGCGAGAAAAAATAGTCTCGATTAAGACCTTCTTGGAAAGAGATAATAA 1321
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QY 1322 GAACGGGGCGTGGGTAATCTGAAAAAATCTATCTTTAATAAGATTAATGAAT 1381
DB 1206 GAACGGGGCGTGGGTAATCTGAAAAAATCTATCTTTAATAAGATTAATGAAT 1265
QY 1382 TATCTCACTTTGGCAGCAGCTGCTCGGATTAAGTCCAGCGGCTCAGCATTTGGTTAGCC 1441
DB 1266 TATCTCACTTTGGCAGCAGCTGCTCGGATTAAGTCCAGCGGCTCAGCATTTGGTTAGCC 1325
QY 1442 AAAAAACAATCTGATGATTTATTCATCAGGTTTAACTTAACTGATTAAGACACTGA 1501
DB 1326 AAAAAACAATCTGATGATTTATTCATCAGGTTTAACTTAACTGATTAAGACACTGA 1385
QY 1502 ACCGTTTCATTCAGAAATATGATTCAGTGAAGCAAGCTGCTAGATGACAGCTTGTA 1561
DB 1386 ACCGTTTCATTCAGAAATATGATTCAGTGAAGCAAGCTGCTAGATGACAGCTTGTA 1445
QY 1562 AATGA 1566
DB 1446 AATGA 1450

RESULT 3
YEPLCR
LOCUS
DEFINITION
ACCESSION
NID
VERSION
KEYWORDS
SOURCE
ORGANISM

YEPLCR 2100 bp DNA BCT 26-APR-1993
Yersinia pestis lcrG, lcrV, and lcrH genes, complete cds.
M26405 9155448
M26405.1 GI:155448
lcrG protein; lcrH protein; lcrV protein; V antigen.
75kb virulence plasmid.
Yersinia pestis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

SOURCE secretion: V antigen; virulence: ylp; yop: ysc.
 ORGANISM Yersinia pestis.
 Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae; Yersinia.

REFERENCE 1 (bases 1 to 70305)
 AUTHORS Karlyshev,A.V. and Wren,B.W.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 70305)
 AUTHORS Baker,S.G. and Mungall,K.
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 70305)
 AUTHORS James,K.D., Parkhill,J., Barrell,B.G. and Randalream,M.A.
 JOURNAL Direct Submission
 Submitted (03-SEP-1999) Yersinia pestis sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA
 E-mail: barrell@sanger.ac.uk DNA supplied by Dr. Andrey Karlyshev and Prof. Brendan Wren, [3]. Department of Infectious and Tropical Diseases, London School Of Hygiene and Tropical Medicine, Keppel Street, London WC1E 7HT

COMMENTS Notes:
 Yersinia pestis sequencing at The Sanger Centre is funded by Becuulf Genomics
 Details of Y. pestis sequencing at the Sanger Centre are available on the World Wide Web.
 (URL: http://www.sanger.ac.uk/Projects/Y_pestis/)
 CDS are numbered using the following system eg YPCP1.01c. yp (Y. pestis), PCP1 (plasmid name), .01 (first CDS), c (complementary strand).
 The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
 The length in codons is given for each CDS.
 Usually the highest scoring similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
 CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (atc) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
 Location/Qualifiers
 1. .70305
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 /plasmid="PCD1"
 /strain="CO-92 Biovar Orientalis"
 /db_xref="taxon:632"
 1. .1956
 /note="IS100 element"
 88. .1110
 /gene="YPCD1.01"
 88. .1110
 /gene="YPCD1.01"
 repeat_unit
 /note="YPCD1.01, probable transposase, len: 340 aa; putative insertion sequence IS100, identical to corresponding CDS from Y.pestis KIM5 PCD1 (EMBL:AF053946, AF074612) (340 aa). fasta scores: opt: 2328 z-score: 3808.9 E(): 0, 100.0% identity in 340 aa overlap. Similar to many others e.g. TRA0_ECOLI (EMBL:X14793), ISfA, E.coli transposase for insertion sequence element IS21 (390 aa) (33.1% identity in 329 aa overlap). Contains Pfam match to entry PF00239 recombinase, site-specific recombinases, score 25.70, E-value 4.8e-06. Contains probable helix-turn-helix motif at aa 19-40 (Score 2045, +6.15 SD)"
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misc_feature
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 /db_xref="gi:5832425"
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 1434. .1457
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 /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
 complement(1956. .2204)
 /partial
 /gene="YPCD1.03c"
 /note="YPCD1.03c, probable transposase remnant, len: 83 aa; similar to several e.g. N-terminus of TRA0_ECOLI (EMBL:X14793), ISfA, E.coli transposase for insertion sequence element IS100 element. The remainder of this CDS is in YPCD1.97c. This region is also similar to TR:068707 (EMBL:AF053946, AF074612) Y.pestis KIM5 putative transposase in PCD1 (390 aa). Contains probable helix-turn-helix motif at aa 19-40 (Score 1833, +5.43 SD)"
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 1956. .46271
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 complement(1956. .2204)
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 /gene="YPCD1.04"
 2304. .2948
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 /gene="YPCD1.04"
 /note="YPCD1.04, possible transposase remnant, len: 215

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aa: similar to many e.g. TR:Q46612 (EMBL:X78052)
Enterobacter agglomerans IS 1222 ORFb (276 aa). Truncated
at N-terminus"
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HMFSDVSHARKTISEMRKODINECRPHSLTYQTPSEFAAAMKRGNSDSSESDITK"
2304..2392
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/gene="ypcd1.05c"
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/notice="ypcd1.05c, syce, yera, yope targeting protein, len:
130 aa: identical to corresponding CDS from Y.pesilis KIM5
PCD1 (EMBL:AF053946, AF074612) (130 aa), fasta scores:
opt: 861 z-score: 1608.5 E(): 0, 100.0% identity in 130 aa
overlap and to YERA_YERPE (EMBL:M34279) from Y.pesilis
plasmid pYV019. Highly similar to TR:Q56910 (EMBL:Z18539),
syce, from Yersinia enterocolitica (130 aa) (99.2%
identity in 130 aa overlap) and YERA_YEREN (EMBL:M34278),
yere, also from Y.enterocolitica (110 aa) (98.5% identity
in 130 aa overlap). Similar to TR:Q51448 (EMBL:L27629),
ORF1, Pseudomonas aeruginosa exoenzyme S ORF1 (116 aa)
(44.3% identity in 115 aa overlap)"
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/translacion="MYSFEGATIQOLFQOOLSIPDTIEPIYKVGSEFCHTEHYRG
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3600..4259
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Best Local Similarity 99.9%: Pred. No. 3.5e-204;
Matches 980: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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|||||
Db 22915 ATGATTAGAGCTCGAACAACCAACCAACATTTTATGAGATCTAGAAAAGTTAGG 22956
OY 646 GTGGAACAACCTACTGTCATGTTCTTCACGTTTATAGAGATGCTCAGTTAGTCAAA 705
|||||
Db 22855 GTGGAACAACCTACTGTCATGTTCTTCACGTTTATAGAGATGCTCAGTTAGTCAAA 22796
OY 706 GATAAAAATATAGATATTTTCATTAAATATGATCCCGAGAAAAGATTGGAGCTTTTGGC 765
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Db 22795 GATAAAAATATAGATATTTTCATTAAATATGATCCCGAGAAAAGATTGGAGCTTTTGGC 22736
OY 766 AATGAGAAATTAAGTATGATGATGAAATGCTCAAGAAAACCTAGCTTATTTCTACCC 825
|||||
Db 22735 AATGAGAAATTAAGTATGATGATGAAATGCTCAAGAAAACCTAGCTTATTTCTACCC 22676
OY 826 GAGGATGATTTCTTAAAGCGGTCATTATGACAACCACTGCAAAAATGGCATCAAGGA 885
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Db 22675 GAGGATGATTTCTTAAAGCGGTCATTATGACAACCACTGCAAAAATGGCATCAAGGA 22616
OY 886 GTAAAAAGATTCTTGATCATCGCCGCAATACACAAATGGGAATTCGGGGCGTTGATGCA 945

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|||||
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OY 946 GTAAATGATTTCTCTTAAACCGCGATCGTATGATGATATATTTTGAAGGATTTGT 1005
|||||
Db 22555 GTAAATGATTTCTCTTAAACCGCGATCGTATGATGATATATTTTGAAGGATTTGT 22496
OY 1006 GATTCAATGATCATCATGCTGATGCCCGTAGCAAGTTCGGTGAAGATTTAGCTGACCT 1065
Db 22495 GATTCAATGATCATCATGCTGATGCCCGTAGCAAGTTCGGTGAAGATTTAGCTGACCT 22436
OY 1066 ACCGCCAATTAAGATTTTTCAGTTATTCACAGCCGAATTTATAGCATCTGCTAGT 1125
Db 22435 ACCGCCAATTAAGATTTTTCAGTTATTCACAGCCGAATTTATAGCATCTGCTAGT 22376
OY 1126 AGTGCACCAATTAATATCCATGATTAATATCATTTATCTGATGATAAAATTTATATGT 1185
Db 22375 AGTGCACCAATTAATATCCATGATTAATATCATTTATCTGATGATAAAATTTATATGT 22316
OY 1186 TATACAGATGAAGAGATTTTAAAGCCAGCGCAGAGTACAAATTTCTGAGAAAATGCGCT 1245
Db 22315 TATACAGATGAAGAGATTTTAAAGCCAGCGCAGAGTACAAATTTCTGAGAAAATGCGCT 22256
OY 1246 CAATCCCATTCAGTGTGATGGGAGCGAGAAAAAATAGTCTGATTAAGGACTTTCTT 1305
Db 22255 CAATCCCATTCAGTGTGATGGGAGCGAGAAAAAATAGTCTGATTAAGGACTTTCTT 22196
OY 1306 GGAAGTGAATTAAGAACACGGGGCGTGGTATCTGAAAAACATCTCTTTATAT 1365
Db 22195 GGAAGTGAATTAAGAACACGGGGCGTGGTATCTGAAAAACATCTCTTTATAT 22136
OY 1366 AAGATTAATATGATTAATATCTCACTTTGCGACACCTGCTCGGATTAAGTCCAGCGCTC 1425
Db 22135 AAGATTAATATGATTAATATCTCACTTTGCGACACCTGCTCGGATTAAGTCCAGCGCTC 22076
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AF053946
LOCUS AF053946 70504 bp DNA circular BCT 06-OCT-1998
DEFINITION Yersinia pestis plasmid pCD1, complete plasmid sequence.
ACCESSION AF053946
NID 92996222
VERSION AF053946.1 GI:2996222
KEYWORDS
SOURCE
ORGANISM
Yersinia pestis.
Yersinia pestis.
Bacteria: Proteobacteria: gamma subdivision: Enterobacteriaceae:
Yersinia.
1 (bases 1 to 70504)
Hu, P., Elliott, J., McCreedy, P., Skowronski, E., Garnes, J.,
Kobayashi, A., Brubaker, R. R. and Garcia, E.
Structural organization of virulence-associated plasmids of
Yersinia pestis
J. Bacteriol. 180 (19), 5192-5202 (1998)
JOURNAL
MEDLINE 98422474
REFERENCE 2 (bases 1 to 70504)
Hu, P., Elliott, J., McCreedy, P., Skowronski, E., Garnes, J.,
Kobayashi, A., Carrano, A. V., Brubaker, R. and Garcia, E.
Direct Submission
Submitted (16-MAR-1998) Biology and Biotechnology, Lawrence
Livermore National Lab, L452, 7000 East Ave., Livermore, CA 94550,

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LOCUS Yersinia pestis plasmid pCD1, complete plasmid sequence.
DEFINITION AF074612
ACCESSION AF074612
VERSION 93822037
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KEYWORDS Yersinia pestis.
SOURCE Yersinia pestis.
ORGANISM Yersinia pestis.
REFERENCE 1 (bases 1 to 70559)
AUTHORS Perry,R.D., Straley,S.C., Fetherston,J.D., Rose,D.J., Gregor,J. and Blattner,F.R.
TITLE DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia pestis KIM5
JOURNAL Infect. Immun. 66 (10), 4611-4623 (1998)
MEDLINE 98427122
REFERENCE 2 (bases 1 to 70559)
AUTHORS Perry,R.D., Straley,S.C., Fetherston,J.D., Rose,D.J., Gregor,J. and Blattner,F.R.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1998) Microbiology and Immunology, University of Kentucky, MS415 Medical Center, Lexington, KY 40536-0084, USA
COMMENT Unique identifiers, starting at Y0001, are assigned to each gene of pCD1.
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DEFINITION	A46413		
ACCESSION	g2300614		
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VERSION			
KEYWORDS	Yersinia pestis.		
SOURCE	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
ORGANISM	Yersinia.		
REFERENCE	1 (bases 1 to 1014)		
AUTHORS	Tilball,R.W., Williamson,E.D. and Leary,S.E.		
TITLE	VACCINE COMPOSITIONS		
JOURNAL	Patent: WO 9524475-A 3 14-SEP-1995;		
COMMENT	SECR DEFENCE BRIT (GB)		
FEATURES	Other publication AU 1853995 950925.		
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DEFINITION	Sequence 3 from Patent WO9628551.		PAT
ACCESSION	A56795		03-MAR-1998
VERSION	A56795.1	GI:3712810	

KEYWORDS Yersinia pestis.
SOURCE Yersinia pestis.
ORGANISM Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae; Yersinia.
REFERENCE 1 (bases 1 to 1014)
AUTHORS Titball, R.W., Williamson, E.D., Leary, Sophie, E.C., Oyston, P.C., Bennett and Alice, M.
TITLE VACCINES FOR PLAGUE
JOURNAL Patent: WO 9628551-A 3 19-SEP-1996;
COMMENT SECR DEFENCE (GB)
Other publication ZA 9602036 960716
Other publication AU 4951196 961002.
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BASE COUNT 343 a 184 c 205 g 282 t
ORIGIN

Query Match 62.28; Score 974.8; DB 5; Length 1014;
Best Local Similarity 99.84; Pred. No. 3.8e-203;
Matches 976; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 589 ATTAGAGCCTACGACAAACCCACACATTTTATGAGATCTAGAAAAAGTTAGGCTG 648
DB 13 ATTGAGCCTACGACAAACCCACACATTTTATGAGATCTAGAAAAAGTTAGGCTG 72
QY 649 GAACAACTTACTGTCATGTTCTTCAGTTTAAAGAAATGTTCAAGTAT 708
DB 73 GAACAACTTACTGTCATGTTCTTCAGTTTAAAGAAATGTTCAAGTAT 132
QY 709 AAAAATATAGATATTCATTAATATGATCCGAAAAAGTTGGAAGTTTGGCAAT 768
DB 133 AAAAATATAGATATTCATTAATATGATCCGAAAAAGTTGGAAGTTTGGCAAT 192
QY 769 AGAGTATTTACTGATGATTCGAATTCGTCAGAAATCCAGTTTATTTCTCCCGAG 828
DB 193 AGAGTATTTACTGATGATTCGAATTCGTCAGAAATCCAGTTTATTTCTCCCGAG 252
QY 829 GATGACATTTCTTAAAGCGGTCATTAAGACCAACACTGCAAAATGGATCAACGAGTA 888
DB 253 GATGACATTTCTTAAAGCGGTCATTAAGACCAACACTGCAAAATGGATCAACGAGTA 312
QY 889 AAAGAGTTCCTGAATCATGCGCGAATACACAAATGGAAATTCGGGGCTTCATGGCAGTA 948
DB 313 AAAGAGTTCCTGAATCATGCGCGAATACACAAATGGAAATTCGGGGCTTCATGGCAGTA 372
QY 949 ATGCATTTCTTTTAAACCGCGATCGATGATGATATTTTGAAGATGATTTGAT 1008
DB 373 ATGCATTTCTTTTAAACCGCGATCGATGATGATATTTTGAAGATGATTTGAT 432
QY 1009 TCAATGATCATCATGATGATGCGGTAGCAAGTTGCGTGAAGATTAAGTGAAGTACC 1068
DB 433 TCAATGATCATCATGATGATGCGGTAGCAAGTTGCGTGAAGATTAAGTGAAGTACC 492
QY 1069 GCCGAATTAAGATTTATTCAGTTATTCACCCCAAAATTAATAAGCATCTGCTAGTAGT 1128
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DB 493 GCCGAATTAAGATTTATTCAGTTATTCACCCCAAAATTAATAAGCATCTGCTAGTAGT 552
QY 1129 GGCACCAATAAATATCCATGATGATTAATTCATTCATGATGATTAATTAATGCTTAT 1188
DB 553 GGCACCAATAAATATCCATGATGATTAATTCATTCATGATGATTAATTAATGCTTAT 612
QY 1189 ACAGATGAAGAGATTTTAAAGCCAGCGAGAGTACAAAATTTCTCGAAGAAATGCTCAA 1248
DB 613 ACAGATGAAGAGATTTTAAAGCCAGCGAGAGTACAAAATTTCTCGAAGAAATGCTCAA 672
QY 1249 ACCACCATTCAGTGGATGGAGCGAGAAAATAATGTCGATTAAGACCTTTCTTGA 1308
DB 673 ACCACCATTCAGTGGATGGAGCGAGAAAATAATGTCGATTAAGACCTTTCTTGA 732
QY 1309 AGTGAGATTAAGAAACCGGGCGTGGTGAATCTGAAATACATCTTATTAATTA 1368
DB 733 AGTGAGATTAAGAAACCGGGCGTGGTGAATCTGAAATACATCTTATTAATTA 792
QY 1369 GATTAATTAAGATTAATCTCATCTTGGCCACACCTGCTGGATTAAGTCCAGCGCTCAAC 1428
DB 793 GATTAATTAAGATTAATCTCATCTTGGCCACACCTGCTGGATTAAGTCCAGCGCTCAAC 852
QY 1429 GACTTGGTTGCCAAAAAACAACACTCAGCTCTGATATTTACACAGTTTATTCAGCT 1488
DB 853 GACTTGGTTGCCAAAAAACAACACTCAGCTCTGATTAATTAATTAATTCAGCT 912
QY 1489 ATTGAACACTGACCGTTTCATTCAGAAATATGATTCAGTATGCAAGCTGCTAGAT 1548
DB 913 ATTGAACACTGACCGTTTCATTCAGAAATATGATTCAGTATGCAAGCTGCTAGAT 972
QY 1549 GACACGTTCTGTTAATGA 1566
DB 973 GACACGTTCTGTTAATGA 990
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RESULT 11
YPTPIVANT 981 bp DNA BCT 13-MAR-1997
LOCUS Y.pseudotuberculosis V antigen gene.
DEFINITION X96802
ACCESSION X96802
NID 91405834
VERSION X96802.1 GI:1405834
KEYWORDS V antigen.
SOURCE Yersinia pseudotuberculosis.
ORGANISM Yersinia pseudotuberculosis
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae; Yersinia.
REFERENCE 1 (bases 1 to 981)
AUTHORS Roggenkamp, A., Geijer, A.M., Leifritz, L., Kessler, A. and Heesemann, J.
TITLE Passive immunity to infection with Yersinia spp. mediated by anti-recombinant V antigen is dependent on polymorphism of V antigen
JOURNAL Infect. Immun. 65 (2), 446-451 (1997)
MEDLINE 97162308
REFERENCE 2 (bases 1 to 981)
AUTHORS Roggenkamp, A.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology, University of Wuerzburg, Josef-Schneider Strasse 2, 97080 Wuerzburg, FRG
FEATURES
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1. 981
CDS
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BASE COUNT 341 a 174 c 191 g 275 t
ORIGIN

Query Match 61.1% Score 957 DB 1: Length 981
Best Local Similarity 98.5% Pred. No. 2.9e-199;
Matches 966; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Db 1 ATGATTAGAGCTAGCAACAAACCCACACATTTTATTGAGATCTAGAAAAGTTAGG 645
QY 586 ATGATTAGAGCTAGCAACAAACCCACACATTTTATTGAGATCTAGAAAAGTTAGG 645
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QY 646 GTGGAACAACCTACTGCTATGTTCTTCAGTTTGAAGAATTGGTTCAGTTACTCAA 705
Db 61 GTGGAACAACCTACTGCTATGTTCTTCAGTTTGAAGAATTGGTTCAGTTACTCAA 120
QY 706 GATAAAATATAGATATTTCATTAATATGATCCGACAAAAGATTCCGAGGTTTTCGC 765
Db 121 GATAAAATATAGATATTTCATTAATATGATCCGACAAAAGATTCCGAGGTTTTCGC 180
QY 766 AATAGAGTAATTAAGATATGATATGCAAGAAATCCCTAGCTTATTTCTACCC 825
Db 181 AATAGAGTAATTAAGATATGATATGCAAGAAATCCCTAGCTTATTTCTACCC 240
QY 826 GAGATACCAATCTTAAAGCGGTCTATTATGACAAACCACTGCAAAATGGATCAAGCGA 885
Db 241 GAGATACCAATCTTAAAGCGGTCTATTATGACAAACCACTGCAAAATGGATCAAGCGA 300
QY 886 GTAAGAAGTTCCTTGATCATCCGCCAATACACATGGGAATTCGGGCGTTCTAGCA 945
Db 301 GTAAGAAGTTCCTTGATCATCCGCCAATACACATGGGAATTCGGGCGTTCTAGCA 360
QY 946 GTAATGCAATTCCTTGATCAACCGCGATGATGATGATATTTTGAAGTATGTT 1005
Db 361 GTAATGCAATTCCTTGATCAACCGCGATGATGATGATATTTTGAAGTATGTT 420
QY 1006 GATTCATGAATCATCATGTGTGATGCCGTAGCAAGTTGCGTGAAGAAATGACTGAGCTT 1065
Db 421 GATTCATGAATCATCATGTGTGATGCCGTAGCAAGTTGCGTGAAGAAATGACTGAGCTT 480
QY 1066 ACCGCCGAATTAAGATTTATTCATGATTAATTCATGATGATTAATTTATATGCT 1125
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QY 1126 AGTGCACCATTAATATCATGATTAATTCATGATGATTAATTTATATGCT 1185
Db 541 AGTGCACCATTAATATCATGATTAATTCATGATGATTAATTTATATGCT 600
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QY 1246 CAACACCATTCAGGTGATGGAGCGAAGAAAAAATAGTCTGCATTAAGACATTTCTT 1305
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Db 721 GGAAGTGAATTAAGAAACCGGGCGTTGGTAACTGAAAAACTCATCTATTAAT 780
QY 1366 AAAGATAATTAAGATTTATCTCACTTTCCACACACCTCTCGATTAAGTCCAGGCGCTC 1425
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Db 841 AACGACTTGTTAGCCAAAAACAACCTACGCTGTCTGATTAATTAATCA 900
QY 1486 GCTATTGAAGCAGTGAACCGTTTCATTCAGAAATATGATTCAGTGAAGCAGTCTGCTA 1545
Db 901 GCTATTGAAGCAGTGAACCGTTTCATTCAGAAATATGATTCAGTGAAGCAGTCTGCTA 960
QY 1546 GATGACACGCTGCTGAATCA 1566
Db 961 GATGACACGCTGCTGAATCA 981

RESULT 12
YEPLCRGVHP
LOCUS
DEFINITION
Yersinia pseudotuberculosis V-antigen (LcrG, LcrV, LcrH) genes,
complete cds.
ACCESSION
M57893
M57893.1 GI:155456
VERSION
M57893.1
KEYWORDS
V-antigen.
Yersinia pseudotuberculosis (strain YPIII (PIB1) DNA.
SOURCE
Yersinia pseudotuberculosis
ORGANISM
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE
1 (bases 1 to 2201)
Bergman, T., Hakansson, S., Forsberg, A., Norlander, L., Macellaro, A.,
Baeckman, A., Boelin, I. and Wolf-Watz, H.
Analysis of the V antigen lcrGVH-yopBD Operon of Yersinia
pseudotuberculosis: Evidence for a regulatory role of LcrH and LcrV
J Bacteriol. 173, 1607-1616 (1991)
J1154114

FEATURES
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/strain="YPIII(PIB1)"
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gene
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"IISSELELRSQDQKIMG"
FGLVFSVLDDCGIVYITGKRSKSGNIELYDKNSLLIENDIKKYLDEDFHRCIML
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Query Match	59.28	Score 927.4	DB 2	Length 69673	
Best Local Similarity	97.38	Pred. No. 17-193			
Matches 943	Conservative 0	Mismatches 26	Indels 0	Gaps 0	
QY	586	ATGATTAGAGCCCTCGAACAACCAACACAACTTTATTGAGATCTGAAAAAGTTAGG	645		
Db	18679	ATGATTAGAGCCCTCGAACAACCAACACAACTTTATTGAGATCTGAAAAAGTTAGG	18620		
QY	646	GTGAAACACCTTACTGGTCATGCTTCTCACTTTTAGAAGAAATGGTTCAGTTACTCAA	705		
Db	18619	GTGAAACACCTTACTGGTCATGCTTCTCACTTTTAGAAGAAATGGTTCAGTTACTCAA	18560		
QY	706	GATAAAAATATAGATATTTTCATTAAATATATGCCAATAAAGATTGGAGGTTTTC	765		
Db	18559	GATAAAAATATAGATATTTTCATTAAATATATGCCAATAAAGATTGGAGGTTTTC	18500		
QY	766	AATAGATATTTACTGATGATATGCAATTCCTCAAGAAATCTGACTTATTTTCTACCC	825		
Db	18499	GATAGGTAATTTACTGATGATATGCAATTTACTCAAGAAATCTGACTTATTTTCTACCC	18440		
QY	826	GAGATACCATTTCTTAAAGCGGCTATATATGACAAACACTGCAAAATGCGATCAAGCA	885		
Db	18439	GAGATGTCATTTTAAAGCGGCTATATATGACAAACACTGCAAAATGCGATCAAGCA	18380		
QY	886	GTAAGAAGTTCCTTGAATCATCGCCGAATACACAAATGGGAATTCGGGCGTTCAGCA	945		
Db	18379	GTAAGAAGTTCCTTGAATCATCGCCGAATACACAAATGGGAATTCGGGCGTTCAGCA	18320		
QY	946	GTAATGCAATTCCTTTAACCGCGCATGTAATGATATTTTGAAGTGATTTGT	1005		
Db	18319	GTAATGCAATTCCTTTAACCGCGCATGTAATGATATTTTGAAGTGATTTGT	18280		
QY	1006	GATTCATGATTCATCATGATGATGCGCGTGCAGATGGCGGAATTTAGTACTAGCTT	1065		
Db	18259	GATTCATGATTCATCATGATGATGCGCGTGCAGATGGCGGAATTTAGTACTAGCTT	18200		
QY	1066	ACCGCCGAATTTAAAGATTATTTCACTAGTATTTGAAGCGCAATTTAATACATCTGCTAGT	1125		
Db	18199	ACCGCCGAATTTAAAGATTATTTCACTAGTATTTGAAGCGCAATTTAATACATCTGCTAGT	18140		
QY	1126	AGTGGCACCATTAATTCATGATTAATTCATTAATCTCATGATAAAAATTATATGCT	1185		
Db	18139	AGTGGCACCATTAATTCATGATTAATTCATTAATCTCATGATAAAAATTATATGCT	18080		
QY	1186	TATACAGTATGAAGATTTTAAAGCCAGCGAGGTGCAAAATCTCGAGAAATAGCT	1245		
Db	18079	TATACAGTATGAAGATTTTAAAGCCAGCGAGGTGCAAAATCTCGAGAAATAGCT	18020		
QY	1246	CAAAACACCATTTAGGTGATGAGAGCAGAAAAAAATAGTCTCGATTAAGGACTTTCTT	1305		
Db	18019	CAAAACACCATTTAGGTGATGAGAGCAGAAAAAAATAGTCTCGATTAAGGACTTTCTT	17960		
QY	1306	GGAAGTGAATTAAGAAGACCGGGCGTGGGTATCTGAAAAACTCATCTTATATAT	1365		
Db	17959	GGAAGTGAATTAAGAAGACCGGGCGTGGGTATCTGAAAAACTCATCTTATATAT	17900		
QY	1366	AAAGATTAATTAATTAATTCATCTTCACCTTGCACACCTGCTGGATAAGCCAGCGCGTC	1425		
Db	17899	AAAGATTAATTAATTAATTCATCTTCACCTTGCACACCTGCTGGATAAGCCAGCGCGTC	17840		
QY	1426	AACGACTTGGTTAGCCAAAAACAACACTGCTGCTGATTTACATCAAGTTTATTTCA	1485		
Db	17839	AACGACTTGGTTAGCCAAAAACAACACTGCTGCTGATTTACATCAAGTTTATTTCA	17780		
QY	1486	GCTATTTGAAGCACTGAACCGTTTCACTTACAGAAATATGATTCAGTATGACAGCTGTGCTA	1545		
Db	17779	GCTATTTGAAGCACTGAACCGTTTCACTTACAGAAATATGATTCAGTATGACAGCTGTGCTA	17720		

QY	1546	GATGACACG	1554
Db	17719	GATGACACG	17711

RESULT 14			
YE96PVANT			
LOCUS	YE96PVANT	975 bp	DNA
DEFINITION	Y.enterocolitica V antigen gene, strain Y-96-P.		
ACCESSION	X96801		
NID	G1405830		
VERSION	X96801.1	GI:1405830	
KEYWORDS	V antigen.		
SOURCE	Yersinia enterocolitica.		
ORGANISM	Yersinia enterocolitica.		
REFERENCE	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Yersinia.		
AUTHORS	1 (bases 1 to 975)		
TITLE	Roggenkamp, A., Gelger, A.M., Leitritz, L., Kessler, A. and Heesemann, U.		
JOURNAL	Passive immunity to infection with Yersinia spp. mediated by anti-recombinant V antigen is dependent on polymorphism of V antigen		
MEDLINE	Infect. Immun. 65 (2), 446-451 (1997)		
REFERENCE	97162308		
AUTHORS	2 (bases 1 to 975)		
TITLE	Roggenkamp, A.		
JOURNAL	Direct Submission		
	Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology		
	University of Wuerzburg, Josef-Schneider Strasse 2, 97080		
	Wuerzburg, FRG		

FEATURES	Location/Qualifiers
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source	1..975 /db_xref="taxon:630"
source	1..975 /organism="Yersinia enterocolitica (type 0:9)"
source	1..975 /strain="Y-96-P"
source	1..975 /db_xref="taxon:34055"
CDS	1..975 /codon_start=1 /transl_table=1 /product="Y antigen" /protein_id="CA65593.1" /db_xref="PID:e239988" /db_xref="PID:g1405831" /db_xref="GI:1405831" /translation="MIRAYEONRPHFGIDLEKRVADQLTGSGSVLEELVYOVQKK DISKIDYDQKSEVYFADRVITDDILELLKILATYLPEDAILKGGATVDQLOGLKRV EFLSSPSYQWLELAFMAVVMHFSLTADIDDDILKVIYDSNMHHQDAGKAELELAE TAEIKLSIVIOALEINKHLSNDDTINIHDKSINLMDKLVNGYDEEIPFASAEYKLE MPQTIKEGTEPERKIVSINKPLESENKPTGALGNLKDYSYKNQDNELSHGTCSDSD SRPLNDIVSQKTTQLOLSDITSFNSIETELNFINFKYDVMQRLDDTR"
BASE COUNT	335 a 177 c 194 g 269 t
ORIGIN	
Query Match	58.5%; Score 916.2; DB 1; Length 975;
Best Local Similarity	96.6%; Pred. No. 2.3e-190;
Matches 936; Conservative	0; Mismatches 33; Indels 0; Gaps 0
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DB	1 AGATTAGAGCTACGAGACAAAACCCCAACACTTTTATTGAGGAGATCTAAGAAAAAGTTAGG 60
QY	646 GTGGAACAACCTACTGCGATCGTCTCTTCAGATTAGAGAATTTGGTTCAGTTAGTCAAA 705
DB	61 GTGGAACAACCTACTGCGATCGTCTCTTCAGTTAGAGAATTTGGTTCAGTTAGTCAAA 120
QY	706 GATAAAATATATGATATTTCCATTAATATGATCCAGAAAAGATTCGAGGATTTTGGC 765
DB	121 GATAAAAGATATGATATTTCCATTAATATGATCCCAAAAAGATTCGAGGATTTTGGC 180

[illegible]

FEATURES	Source	Location/Qualifiers
JOURNAL	Passive immunity to infection with Yersinia spp. mediated by anti-recombinant V antigen is dependent on polymorphism of V antigen	
MEDLINE	Infect. Immun. 65 (2), 446-451 (1997)	
REFERENCE	97162308	
AUTHORS	2 (bases 1 to 975)	
TITLE	Rogenkamp, A.	
JOURNAL	Direct Submission	
	Submitted (22-MAR-1996) A. Rogenkamp, Hygiene und Microbiology, University of Wuerzburg, Josef-Schneider Strasse 2, 97080 Wuerzburg, FRG	
BASE COUNT	341 a 173 c 190 g 271 t	
ORIGIN		
Query Match	58.4%; Score 914.6; DB 1; Length 975;	
Best Local Similarity	96.5%; Pred. No. 5.2e-190;	
Matches 935; Conservative 0; Mismatches 34; Indels 0; Gaps 0;		
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301 GTAAAAAGATTCCTTGATCATCGCCGCAATACACAAATGGGAATTCGGGCGTTTCATGGCA 360		
946 GTAATGCATTTCTCTTTAACCGCGATCGTATCGATGATGATATTTTGAAGATGATTGTT 1005		
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1006 GATTCAATGATTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1065		
421 GATTCAATGATTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480		
1066 ACCCGCGAATTAAGATTTATTCAGTATTTTCAACCGCAAAATTAATAGCATCTGTAGT 1125		

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Db 481 ACCGCCGAATTTAAATTTATTCAGTTATTCAGCTGAATTAATTAAGCATCTGCGAAT 540
OY 1126 AGTGGACCATTAATATTCATGATTAATCCATTAATCTCATGATTAATAATTTATATGT 1185
Db 541 AGTGACACCATTAATATTCATGATTAATCAATTAATCTCATGATTAATAATTTATATGT 600
OY 1186 TATACAGATGAAGAGATTTTAAAGCCAGCGCAGAGTACAAAATTCGAGAAAATGCTT 1245
Db 601 TATACAAATGAAGAGATTTTAAAGCCAGCGCAGAGTACAAAATTCGAGAAAATGCTT 660
OY 1246 CAATCCACCATTTAGTGGATGGAGCGAGAAAATACTCTGATTAAGACTTTCTT 1305
Db 661 CAATCCACCATTTAGAGGTGAGACCGAATAAATAGTCTGATTAAGAACTTTCTT 720
OY 1306 GGAAGTGAGATTAAGAAACCGGGCGTTGGTATCTGAATAAAGTATCTTATAT 1365
Db 721 GAAAGTGAGATTAAGAAACCGGGCGTTGGTATCTGAATAAAGTATCTTATAT 780
OY 1366 AAAGATTAATGAATTAATCTCACTTGGCAGCAGCTGCTGGATTAAGTCCAGCGGCTC 1425
Db 781 AAAGATTAATGAATTAATCTCACTTGGCAGCAGCTGCTGGATTAAGTCCAGCGGCTC 840
OY 1426 AAGCACTTGTAGCCAAAAACAACACTCAGCTCTGATATTACATCAGCTTTAATCA 1485
Db 841 AAGCACTTGTAGCCAAAAACAACACTCAGCTCTGATATTACATCAGCTTTAATCA 900
OY 1486 GCTATTGAAGCACTGAACGTTTCATTCAGAAATATGATTCAGTGAAGCTGCTA 1545
Db 901 GCTATTGAAGCACTGAACGTTTCATTCAGAAATATGATTCAGTGAAGCTGCTA 960
OY 1546 GATGACACG 1554
Db 961 GATGACACG 969
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 27, 1999, 17:32:44 ; Search time 305.3 Seconds
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12015.090 Million cell updates/sec

Title: US-08-699-716A-1
Perfect score: 1566
Sequence: 1 ATGGGCCATCATCATCATCA.....ATGACACGTCTGGTAATGA 1566

Scoring table: IDENTITY_NOC

Searched: 3032314 segs, 1171202697 residues

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2: em_est2: *
3: em_est3: *
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52: em_est52: *
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62: em_est30: *
63: em_est31: *
64: em_est32: *
65: em_est33: *
66: em_est34: *
67: em_est35: *
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69: em_est37: *
70: em_est38: *
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73: em_est41: *
74: em_est42: *
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91: em_est59: *
92: em_est60: *
93: em_est61: *
94: em_est62: *
95: em_est63: *
96: em_est64: *
97: em_est65: *
98: em_est66: *
99: em_est67: *
100: em_est68: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	41.8	2.7	579	44	AU038989	AU038989 AU038989
2	41	2.6	444	24	H78200	H78200 yu84f10.r1
3	40.8	2.6	561	40	C91275	C91275 C91275 Dict
4	40.6	2.6	394	25	N97614	N97614 1054C3 czap
5	39	2.5	510	39	C84881	C84881 C84881 Dict
6	38.6	2.5	1107	31	C22922	C22922 C22922 Dict
7	38.6	2.5	526	63	AM004525	AM004525 701932008
8	38.6	2.5	489	64	AL121551	AL121551 DKF26762L
9	38	2.4	243	35	AA547782	AA547782 EST188681
10	37.8	2.4	469	62	AU076358	AU076358 AU076358
11	37.4	2.4	640	26	W95009	W95009 zh46d04.r1
12	37.4	2.4	685	50	AU061085	AU061085 AU061085
13	37.2	2.4	506	61	AI808691	AI808691 w57408.x
14	37	2.4	229	35	AA547780	AA547780 EST188689
15	37	2.4	496	44	AU037010	AU037010 AU037010
16	36.8	2.3	382	29	AA143875	AA143875 MCC60261.
17	36.8	2.3	249	35	AA547759	AA547759 EST188668
18	36.8	2.3	239	35	AA547760	AA547760 EST188669
19	36.6	2.3	270	35	AA547784	AA547784 EST188693
20	36.4	2.3	588	35	AA550687	AA550687 1924m3 gm
21	36.4	2.3	689	64	AL119439	AL119439 DKF2P761K
22	36.2	2.3	424	20	D29133	D29133 HDNKK157 Hu
23	36.2	2.3	401	37	AA668776	AA668776 aa80b10.s
24	36.2	2.3	422	59	AI775965	AI775965 EST257065
25	36.2	2.3	522	59	AI776377	AI776377 EST257477
26	36	2.3	229	28	AA114611	AA114611 mn04c03.r
27	36	2.3	625	44	AU037754	AU037754 AU037754
28	36	2.3	327	44	AU037911	AU037911 AU037911
29	35.8	2.3	480	22	H09719	H09719 y190b12.s1
30	35.8	2.3	573	39	AA894968	AA894968 vx65c06.r
31	35.6	2.3	421	35	C24612	C24612 C24612 Dict
32	35.6	2.3	384	40	AA978194	AA978194 OP33d03.S
33	35.6	2.3	291	44	AU039780	AU039780 AU039780
34	35.4	2.3	400	20	T09814	T09814 0401m3 gmbp
35	35.4	2.3	267	20	T18170	T18170 0770C3 czap
36	35.4	2.3	221	35	AA547786	AA547786 EST188695
37	35.4	2.3	406	40	AA975418	AA975418 cn59g12.s
38	35.4	2.3	433	41	AI027570	AI027570 oy46c06.x
39	35.4	2.3	409	43	AI186323	AI186323 qd25h10.x
40	35.4	2.3	405	44	AI279748	AI279748 qp28a09.x
41	35.4	2.3	566	46	AI421821	AI421821 lf55b04.x
42	35.4	2.3	431	50	AI673292	AI673292 tw69g08.x
43	35.4	2.3	657	63	AI935161	AI935161 wp14d12.x
44	35.4	2.3	569	64	AW052061	AW052061 wx25b04.x
45	35.2	2.2	435	22	R80620	R80620 y196f09.r1

ALIGNMENTS

RESULT	1
AU038989	
LOCUS	AU038989 579 bp mRNA EST 29-MAR-1999
DEFINITION	AU038989 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
ACCESSION	AU038989
NID	93985742
VERSION	AU038989.1 GI:3985742
KEYWORDS	EST
SOURCE	Dictyostelium discoideum.
ORGANISM	Dictyostelium discoideum
REFERENCE	Eukaryota; Dictyostelida; Dictyostelium.
AUTHORS	1 (bases 1 to 579)
	Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
	Yoshino,R., Mita,B.N., Pl.M., Sato,T., Takemoto,K., Yashikawa,H.,
	Williams,J., Maeda,M., Takeuchi,T., Ochiai,H. and Tanaka,Y.
	The Dictyostelium developmental cDNA project: generation and
	analysis of expressed sequence tags from the first-finger stage of
	development
JOURNAL	DNA Res. 5 (6), 335-340 (1998)
MEDLINE	99156227
COMMENT	On Jan 19, 1998 this sequence version replaced gi:2150712.

FEATURES
source
1. 579
location/Qualifiers
PROJECT = 'Dictyostelium discoideum CDNA project in Japan'.
Email: da02huesakura.cc.tsukuba.ac.jp
University of Tsukuba
3-3-10 Ten-noda1, Tsukuba, Ibaraki 305, Japan
Institute of Biological Sciences
Contact: Hideko Urushihara
Institute of Biological Sciences

```

/organism="Dicyoscellium discoidum"
/strain="AY4"
/db_xref="taxon:44689"
/map="2: 21q"
/clone="SSM246"
/clone_lib="dictyostelium discoidum SS (H. Urushihara)"
/dev_stage="slug"
BASE COUNT      286 a      31 c      52 g      210 t
ORIGIN

```

Query Match	2.7%	Score 41.8;	DB 44;	Length 579;
Best Local Similarity	45.0%;	Pred. No. 1.4;		
Matches 157;	Conservative 0;	Mismatches 199;	Indels 0;	Gaps 0;

QY 970 GATCGTATCGATGATGATATTTTGAAGGATGTGGATTCATTAATCATCATGCTGT 1029
Db 71 GGTCTATTTTTTGGATGAAAATATTTATTAATTAATCAATAGTAATTAATTAATTAATGCGAT 130
QY 1030 GCCCGTAGCAAGTCCGTGAGCAAGATTAGCTGAGCTACCGCCGAAATTAAGAATTTATTCA 1089
Db 131 GATGATGATGATTAATAAATGAGACAGACATGATGATTAATTAATTAATTAATTAATTAAT 190
QY 1090 GTTATTCAGCCGGAATTAATTAAGCATCTGTCTAGTAGTGGCACCATAATATTCATGAT 1149
Db 191 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 250
QY 1150 AATATTCATTAACTCTCATGATTAATAATTTATATGTGTTATACGATGAGAGATTTTAA 1209
Db 251 AATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTAAAT 310
QY 1210 GCCACCGCGAGATACAAAATTTCTCGAGAAAATGCCCTCAACACCATTTAGTGGATGG 1269
Db 311 TGGATTTAAACAATGTAATCATATATCATCAATCAATTTTCATTAATTAATTAATTAAGAAGTCT 370
QY 1270 AGCGAGAAAAAATATAGCTCGATTAAGGACCTTTCTGGAAGTGAATA 1318
Db 371 ATGAACACAAGGTGTTTATTTAAATAATGAATTAATTAATTAATTAATGA 419

RESULT	2
H78200	
LOCUS	
DEFINITION	H78200 444 bp mRNA EST 09-NOV-1995
IMAGE:240523.5	Similar to gb M87923 HOMALU016 Human carcinoma cell-derived Alu RNA transcript, (rRNA): gb:M57627 INTERLEUKIN-10 PRECURSOR (HUMAN); contains Alu repetitive element., mRNA sequence.
ACCESSION	H78200
NID	q1056289
VERSION	H78200.1 GI:1056289
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryote:	Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria;	Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1 (bases 1 to 444)
AUTHORS	Hallier,L., Clark,N., Dubouche,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,D., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Tveitaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE	The Mashu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	On Apr 14, 1993 this sequence version replaced gi:692889.

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel.: 314 286 1800
 Fax: 314 286 1810
 Email: estwatson.wustl.edu
 Insert Size: 1655
 High quality sequence stops: 342
 Source: IMaG Consortium, LNLN
 This clone is available royalty-free through LNLN; contact the
 IMaG Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1655 Std Error: 0.00
 Seq primer: M13RPI
 High quality sequence stop: 342.
 Location/Qualifiers
 1..444

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BASE COUNT      96 a      101 c      90 g      150 t
ORIGIN
//sample="GDB:378956"
//db_xref="taxon:9606"
//clone_image:240523"
/clone_id="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pTR73D (Pharmacia)
with a modified polylinker. Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - Oligo(dT) primer
[5' AACGCGACGATGTAATTAAAGATCTTTTCTTTTCTTTTCTT 3'] ,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia) , digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pTR73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fátima Bonaldo."

```

Query Match	2.6%	Score 41	DB 24	Length 444
Best Local Similarity	60.2%	Pred. No. 2.2		
Matches 68	Conservative	0	Mismatches 45	Indels 0
				caps 0
QY 1081	ATTATTCAGTTATTCAGCCGAATTAATTAAGCATCTGTCTAGTAGTGCCACCATTAAT	1140		
Db 193	ATTATTCAGTCATTCCTCAAGAGTATTGAATGAGCATCTGCCAGGCGCTGGAATGTTGAT	252		
QY 1141	ATTCAGTAAATCATTAATTCATGATGAATAAATTTATTTGGTTATACAGA	1193		
Db 253	AACACTGCTTATTTATTTTACTTATTTATTTATTTATTTATTTTGACACACA	305		

[illegible][illegible]

```

BASE COUNT,      507 a      121 c      194 g      285 t
ORIGIN           /clone_lib="Dictyostelium discoideum FC (H. Urushihara)"

```

FEATURES	
source	<p>1. .526</p> <p>/organism="Arabidopsis thaliana"</p> <p>/db_xref="taxon:3702"</p> <p>/map="2"</p> <p>/clone="701932008"</p> <p>/clone_1b="A. thaliana, mixed source"</p> <p>/note="This sequence was obtained from a clone generated with a PCR product of the target gene."</p>
BASE COUNT	180 a 118 c 130 g 98 t
ORIGIN	

[illegible]

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 640)
AUTHORS	Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissee,S., Dietrich,N., Dubaque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Roehlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE	Generation and analysis of 280,000 human expressed sequence tags
JOURNAL	Genome Res. 6 (9), 807-828 (1996)
MEDLINE	97044478
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (infoimage.llnl.gov) for further information. Insert Length: 1189 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 440. Location/Qualifiers 1..640 /organism="Homo sapiens" /db_xref="GDB:1133581" /db_xref="taxon:9606" /clone="IMAGE:415111" /clone_id="Soares_fetal_liver_spleen_1NFLS_S1" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /note="Organ: Liver and Spleen; Vector: pTZ193D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a substituted version of the original Soares fetal liver spleen 1NFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer 15' AACGGAAGAATTAAATGAAGACCTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTZ193 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	192 a 128 c 123 g 193 t 4 others
ORIGIN	
Query Match	2.4%; Score 37.4; DB 26; Length 640;
Best Local Similarity	47.6%; Pred. No. 19;
Matches 110; Conservative	0; Mismatches 121; Indels 0; Gaps 0;
Oy	720 TATTTCCTTAATAATGTATCCCAAGAAAGATTCGGAGCTTTTGCCCAATAGAGTAATTAC 779
Db	
Oy	400 TCCTTTTCCAATTGGTTTCTTAACCACAGCTGTATGTCTTCAATTAATAAATAAT 341
Db	
Oy	780 TGATGATATCGAATGTGCACGAANAATCCPTGACTAATTTTTCACCCGGAGATACCATTC 839
Db	
Oy	340 TGATGTTTAAACAGCCTTTTACAATGTTTAAAATGATTTTACTGTATTCGCTAATTTGGA 281
Db	
Oy	840 TAAAGCGGCTATTGACAACCAATCGCAAAATGGCATCAAGCAGATAAAGAGACTTCT 899
Db	
Oy	280 TAATACGGGCGATGCTCTTACACAGCCTTCAGAAATATTTTCAGGCAAGTAAAGAGAGATCC 221
Db	
Oy	900 TGAATCATCGCGGAATACACAATGGAGATTCGGCGCGCTCATCGCAGTAAT 950
Db	
Oy	220 ATTATTAAAGCTGTATAACAGCCTTCACTTTGAAAATTTCAAAGCAGTAT 170
Db	

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056

```

Fax: 3018699423
Email: arkerlav@tigr.org
Seq primer: M13 Reverse.
          location/Qualifiers
source 1. .239

```

BASE COUNT
 ORIGIN
 98 a
 14 c
 25 g
 99 t
 3 others
 was constructed using an oligo-dT primer and directionally
 cloned using the Lambda Zap II Vector Kit by Stratagene.
 EcoRI: Site_2: XhoI: Total RNA was purified from adult
 Note="Organ: brain; Vector: pluscript SK-; Site_1:
 /clone_type="cerebral ganglia"
 /clone_lib="B. glabrata adult cerebral ganglia"
 /map="MMU16C3-C4 region; MMU16C3-C4 region"
 /db_xref="taxon:6526"
 /strain="BS-90"
 /organism="Biomphalaria glabrata"
 1..239
 location/Qualifiers
 Seq primer: M13 Reverse
 Email: arkerlavet@iar.org
 Fax: 3018699423
 FEATURES
 source

[illegible]

RESULT 15				
LOCUS	AU037010	466 bp	mRNA	EST 29-MAR-1999
DEFINITION	AU037010 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium			
ACCESSION	discoidium CDNA clone SSA746, mRNA sequence.			
NID	AU037010			
VERSION	93983763			
KEYWORDS	AU037010.1	GI:3983763		
SOURCE	EST.			
ORGANISM	Dictyostelium discoideum.			
REFERENCE	Dictyostelium discoideum			
AUTHORS	Eukaryota; Dictyostelid; Dictyostelium.			
	1 (bases 1 to 466)			
	Moriio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,			
	Yoshino,R., Mita,B.N., Pl.M., Sato,T., Takemoto,K., Yasukawa,H.,			
	Williams,J., Maeda,M., Takeuchi,T., Ochiai,H. and Tanaka,Y.			
	The Dictyostelium developmental cDNA project: generation and			
	analysis of expressed sequence tags from the first-finger stage of			
	development			
JOURNAL	DNA Res. 5 (6), 335-340 (1998)			
MEDLINE	99156227			
COMMENT	On Jan 17, 1998 this sequence version replaced gi:19000417.			

FEATURES
source
I. .496
Location/Qualifiers
PROJECT = 'dictyostelium discoideum cdna project in japan'.
Email: 'd402huesakura.cc.tsukuba.ac.jp'
University of Tsukuba
3-3-10 Ten-noda1, Tsukuba, Ibaraki 305, Japan
Institute of Biological Sciences
Contact: Hideko Urushihara
Tsukuba

```

/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/map="11; 11, 1.71cR from WI-635"
/clone="SSA746"

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BASE COUNT	266	a	39	c	41	g	147	t	3	others
ORIGIN	/clone_lib="Dictyostellium discoideum SS (H.vrushhara)" /dev_stage="slug"									

	Query Match	2.4%	Score 37	DB 44	Length 496
	Best Local Similarity	47.2%	Pred. No. 23		
	Matches 109	Conservative	0	Mismatches 122	Indels 0
				Gaps	
QY	1089	AGTTATTCAAGCCGAATTATAAGCATCTGTRAGTGGCACCCTAAATTCATGA	1148		
Db	139	AGTTAAATTCATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	198		
QY	1149	TAATTCATTAAATCTCATGATTAATAAATTTATATGGTATACAGATAGAGATTTTAA	1208		
Db	199	TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	258		
QY	1209	AGCCAGGCAGACTACAAATTTCTGAGAAAATGCCCTCAACCACTTCAGGTGATGA	1268		
Db	259	TAATGATATTCGATTTGGAAGCAAAAATGAGATTTTCAACCACTTCCTCAAGAATGT	318		
QY	1269	GAGCGAGAAAATAATGTCTGATTAAGAGACCTTCTTGGAGTGTAGATTA	1319		
Db	319	TAGCGAGCACTGTGAAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA	369		

Search completed: November 27, 1999, 17:50:42
Job time: 1078 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 1999, 18:49:42 ; Search time 43.65 Seconds
(without alignments)
8975.963 Million cell updates/sec

Title: US-08-699-716A-1

Perfect score: 1566

Sequence: 1 ATGGGCCATCATCATCATCA.....ATGACAGCTGTGTAATGA 1566

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1472	94.0	1530	1	Y. pestis F1/V ant
2	1409	90.0	1462	1	Y. pestis F1/V ant
3	976.8	62.4	1014	1	Partial LcrV (V an
4	975.2	62.3	1014	1	Y. pestis lcrV (V
5	974.8	62.2	1014	1	Y. pestis lcrV (V
6	973.2	62.1	1014	1	Partial LcrV (V an
7	517.2	33.0	544	1	Nucleotide sequenc
8	516.8	33.0	547	1	Yersinia pestis ca
9	516.8	33.0	544	1	Y. pestis F1 antiq
10	516.8	33.0	544	1	Nucleotide sequenc
11	510	32.6	544	1	Nucleotide sequenc
12	452.8	28.9	474	1	Nucleotide sequenc
13	452.2	28.9	541	1	Yersinia pestis ca
14	452.2	28.9	541	1	Y. pestis caF1 (F1
15	451	28.8	542	1	Yersinia pestis ca
16	448	28.6	450	1	Nucleotide sequenc
17	447	28.5	447	1	Nucleotide sequenc
18	402	25.7	576	1	Nucleotide sequenc
19	339	21.6	513	1	Nucleotide sequenc
20	68.8	4.4	861	1	sfy anti-rev seque
21	68.8	4.4	861	1	sfy anti-rev seque
22	68.4	4.4	375	1	DNA fragment 2 of
23	68.4	4.4	375	1	DNA fragment 3 of
24	68.4	4.4	375	1	DNA fragment 4 of
25	54	3.4	1546	1	Clostridium botuli
26	53.4	3.4	1402	1	Type A neurotoxin
27	53.4	3.4	1278	1	Chlamydomonas rein
28	53.4	3.4	1469	1	Clostridium botuli
29	53.4	3.4	1460	1	Clostridium botuli
30	53.4	3.4	1535	1	Clostridium botuli
31	53.4	3.4	1526	1	Clostridium botuli
32	53.4	3.4	1547	1	Clostridium botuli
33	53.4	3.4	1463	1	Clostridium botuli
34	53.4	3.4	1472	1	Clostridium botuli
35	53.4	3.4	1502	1	Clostridium botuli
36	53.4	3.4	1402	1	Clostridium botuli
37	46.8	3.0	104	1	Ich-2 gene 5' prim
38	45	2.9	21591	1	Enterococcus faeca
39	42	2.7	110000	1	Continuation (2 of
40	42	2.7	110000	1	Continuation (3 of
41	40	2.6	110000	1	Continuation (16 o
42	39	2.5	4435	1	CCV-C54 spike gene
43	38.8	2.5	1116	1	soybean seed stora

ALIGNMENTS

RESULT	ID	Query Match	Length	ID	Description
1	T38249	94.0	1530	1	Y. pestis F1/V ant
2	T38249	90.0	1462	1	Y. pestis F1/V ant
3	T38249	62.4	1014	1	Partial LcrV (V an
4	T38249	62.3	1014	1	Y. pestis lcrV (V
5	T38249	62.2	1014	1	Y. pestis lcrV (V
6	T38249	62.1	1014	1	Partial LcrV (V an
7	T38249	33.0	544	1	Nucleotide sequenc
8	T38249	33.0	547	1	Yersinia pestis ca
9	T38249	33.0	544	1	Y. pestis F1 antiq
10	T38249	33.0	544	1	Nucleotide sequenc
11	T38249	32.6	544	1	Nucleotide sequenc
12	T38249	28.9	474	1	Nucleotide sequenc
13	T38249	28.9	541	1	Yersinia pestis ca
14	T38249	28.9	541	1	Y. pestis caF1 (F1
15	T38249	28.8	542	1	Yersinia pestis ca
16	T38249	28.6	450	1	Nucleotide sequenc
17	T38249	28.5	447	1	Nucleotide sequenc
18	T38249	25.7	576	1	Nucleotide sequenc
19	T38249	21.6	513	1	Nucleotide sequenc
20	T38249	4.4	861	1	sfy anti-rev seque
21	T38249	4.4	861	1	sfy anti-rev seque
22	T38249	4.4	375	1	DNA fragment 2 of
23	T38249	4.4	375	1	DNA fragment 3 of
24	T38249	4.4	375	1	DNA fragment 4 of
25	T38249	3.4	1546	1	Clostridium botuli
26	T38249	3.4	1402	1	Type A neurotoxin
27	T38249	3.4	1278	1	Chlamydomonas rein
28	T38249	3.4	1469	1	Clostridium botuli
29	T38249	3.4	1460	1	Clostridium botuli
30	T38249	3.4	1535	1	Clostridium botuli
31	T38249	3.4	1526	1	Clostridium botuli
32	T38249	3.4	1547	1	Clostridium botuli
33	T38249	3.4	1463	1	Clostridium botuli
34	T38249	3.4	1472	1	Clostridium botuli
35	T38249	3.4	1502	1	Clostridium botuli
36	T38249	3.4	1402	1	Clostridium botuli
37	T38249	3.0	104	1	Ich-2 gene 5' prim
38	T38249	2.9	21591	1	Enterococcus faeca
39	T38249	2.7	110000	1	Continuation (2 of
40	T38249	2.7	110000	1	Continuation (3 of
41	T38249	2.6	110000	1	Continuation (16 o
42	T38249	2.5	4435	1	CCV-C54 spike gene
43	T38249	2.5	1116	1	soybean seed stora

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Db 191 CAGAACTTCTTGTGGTACGCTTACTCTTGGCGGCTATTAACACAGAACCACTAGACACT 250
Oy 308 CTGTAACTTTACAGATGCCGGGGTGATCCCATGTACTTAACATTACTTCTCAGAGT 367
Db 251 CTGTAACTTTACAGATGCCGGGGTGATCCCATGTACTTAACATTACTTCTCAGAGT 310
Oy 368 GAAATTAACCACTTACTACAAAAGTATGGCAAGATTTCTAGATTTGATATCT 427
Db 311 GAAATTAACCACTTACTACAAAAGTATGGCAAGATTTCTAGATTTGATATCT 370
Oy 428 CTCTTAAGTAACGGTGAACCTTGTGGGGATGACGTCGTTGGTACGGGAGCC 487
Db 371 CTCTTAAGTAACGGTGAACCTTGTGGGGATGACGTCGTTGGTACGGGAGCC 430
Oy 488 AGGATTTCTTTGTGCTCAATTTGGTCCAAAGCGGTAACTTGACAGCATTAATACA 547
Db 431 AGGATTTCTTTGTGCTCAATTTGGTCCAAAGCGGTAACTTGACAGCATTAATACA 490
Oy 548 CTGATGCTGTAAACCGTATCTAACCAAGAAATTCAT-----GATTAGACCT 598
Db 491 CTGATGCTGTAAACCGTATCTAACCAAGAAATTCAT-----GATTAGACCT 550
Oy 599 ACGAACAACCCACACATTTTATGAGATCTAGAAAAGTTAGGGTGAACAACCTA 658
Db 551 ACGAACAACCCACACATTTTATGAGATCTAGAAAAGTTAGGGTGAACAACCTA 610
Oy 659 CTGCTATGCTTCTTCAGTTTATGAGAAGTGTGTACAGTACTCAAGATAAAATATAG 718
Db 611 CTGCTATGCTTCTTCAGTTTATGAGAAGTGTGTACAGTACTCAAGATAAAATATAG 670
Oy 719 AATATTCATTAATATATGATCCAGAAAAGATTCGAGAGTTTGGCAATAGATTA 778
Db 671 AATATTCATTAATATATGATCCAGAAAAGATTCGAGAGTTTGGCAATAGATTA 730
Oy 779 CTGATGATATCAATTTGCTCAAGAAAATCCTAGCTTATTTTACCCGAGTACCATTC 838
Db 731 CTGATGATATCAATTTGCTCAAGAAAATCCTAGCTTATTTTACCCGAGTACCATTC 790
Oy 839 TTTAAGGGGCTATATGACAACAACATGCAAAATGGCATCAAGGAGTAAAGAGTTCC 898
Db 791 TTTAAGGGGCTATATGACAACAACATGCAAAATGGCATCAAGGAGTAAAGAGTTCC 850
Oy 899 TTGAATCATCCCGCAATACACATGGGAATTCGGGGCTTCATGGCAGTAAATGCTTCT 958
Db 851 TTGAATCATCCCGCAATACACATGGGAATTCGGGGCTTCATGGCAGTAAATGCTTCT 910
Oy 959 CTTTACGGCGCATGATCATGATGATATTTGAAAGTGTGTTGATTAAGAAATC 1018
Db 911 CTTTACGGCGCATGATCATGATGATATTTGAAAGTGTGTTGATTAAGAAATC 970
Oy 1019 ATCATGCTGATCCCGTACGAGTATGCGTGAAGAAATTAAGCTAGCTTACCGCCGATTTA 1078
Db 971 ATCATGCTGATCCCGTACGAGTATGCGTGAAGAAATTAAGCTAGCTTACCGCCGATTTA 1030
Oy 1079 AGATTTATTCAGTATTTCAAGCCGAATTAATTAAGCATCTGCTAGTAGTGGCACCATTA 1138
Db 1031 AGATTTATTCAGTATTTCAAGCCGAATTAATTAAGCATCTGCTAGTAGTGGCACCATTA 1090
Oy 1139 AATATCATGATTAATCATTAATCATGATGATTAATTAATTAATGATAGTGAAG 1198
Db 1091 AATATCATGATTAATCATTAATCATGATGATTAATTAATTAATGATAGTGAAG 1150
Oy 1199 AGATTTTAAAGCCAGCGAGATCAAAATTTCTGAGAAAATGCTCAACACCATTC 1258
Db 1151 AGATTTTAAAGCCAGCGAGATCAAAATTTCTGAGAAAATGCTCAACACCATTC 1210
Oy 1239 AGGTGGATGGAGCGAGAAAATATGTCGATAAAGAGCTTTCTTGGAGTGAAGATA 1318
Db 1211 AGGTGGATGGAGCGAGAAAATATGTCGATAAAGAGCTTTCTTGGAGTGAAGATA 1270
Oy 1319 AAGAAGCGGGGCTTGGGTATCTGAANAACATCACTCTATATATAAGTATTAATG 1378
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Db 1271 AAGAAGCGGGGCTTGGGTATCTGAANAACATCACTCTATATATAAGTATTAATG 1330
Oy 1379 AATATCTCACTTTGGCCACACCTGCTCGATTAAGTCCAGGCCGCTCAACGACTGGTTA 1438
Db 1331 AATATCTCACTTTGGCCACACCTGCTCGATTAAGTCCAGGCCGCTCAACGACTGGTTA 1390
Oy 1439 GCCAAAACAACTCAGTGTCTGATTAATACACGTTTAATTAATCACTTTGAAGCAC 1498
Db 1391 GCCAAAACAACTCAGTGTCTGATTAATACACGTTTAATTAATCACTTTGAAGCAC 1450
Oy 1499 TGAACGTTTCAATTCAGAAAATGATTCAGTATGATCAACGCTGCTAGATGACAGCTG 1558
Db 1451 TGAACGTTTCAATTCAGAAAATGATTCAGTATGATCAACGCTGCTAGATGACAGCTG 1510
Oy 1559 GTAANTGA 1566
Db 1511 GTAANTGA 1518

RESULT 2
T38256
ID T38256 standard; DNA; 1462 BP.
AC T38256;
DT 28-DEC-1996 (first entry)
DE Y. pestis F1/V antigen gene fusion.
KW Plague; vaccine; genetic immunisation; V antigen; lcrv;
KW F1 antigen; catl; ds.
OS Chimeric Yersinia pestis strain GB;
FH Key
FT cds location/Qualifiers
FT 8..1450
FT /*tag= a
FT /product= F1/V fusion protein
FT misc_feature 452..472
FT /*tag= b
FT /note= "bases 452-472 is a sequence derived
FT from PCR primers"
FN W09628551.A1.
PD 19-SEP-1996.
PR 13-MAR-1996; G00571.
PR 13-MAR-1995; GB-005059.
PR 15-SEP-1995; GB-018946.
PR 05-DEC-1995; GB-024825.
PA (MTNA ) UK SEC FOR DEFENCE.
PI Bennett AM, Leary SEC, Oyston PCF, Tibball RW, Williamson ED;
DR WPI; 96-433824/43.
DR P-PSDB; W01045.
PT Yersinia pestis V antigen and F1 antigen or their protective
PT epitopic parts - useful in vaccine for protection against plague
PS Disclosure; Page 51-55; 98pp; English.
CC A gene fusion (T38256) comprises coding sequences for the Yersinia
CC pestis F1 antigen (see also T38244) (without the signal sequence)
CC and for the Y. pestis V antigen (see also T38243), joined by a
CC sequence encoding a 6-amino acid peptide linker. It was obtd. by
CC PCR amplification of the individual genes using primers (see also
CC T38245) based on the genes and including linker sequences. The
CC gene fusion (see also T38249) can be used to produce F1/V fusion
CC protein (W01045) in transformed cells, esp. gut-colonising
CC organisms, to induce an immune response against Y. pestis, the
CC causative organism of plague.
SQ Sequence 1462 BP; 476 A; 285 C; 301 G; 400 T;

Query Match 90.0%; Score 1409; DB 1; Length 1462;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1431; Conservative 0; Mismatches 5; Indels 9; Gaps 1;
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Db 66 CTTTACATATAAGSAGGCGCTCCATTACATTTATGGACATGGAAACATCGATACAG 125
QY 251 AATTACTTGTGGTAGCGTTACTCTTGGCGGCTATATAAACAGAGAACCTAGCACATCTG 310
Db 126 AATTACTTGTGGTAGCGTTACTCTTGGCGGCTATATAAACAGAGAACCTAGCACATCTG 185
QY 311 TTAACCTTACAGATGGCGGGGATCCATGATCTTAACATTTACTTCTCAGAGATGGA 370
Db 186 TTAACCTTACAGATGGCGGGGATCCATGATCTTAACATTTACTTCTCAGAGATGGA 245
QY 371 ATAACCCACCAATTCATACAAAAAGATTTGGCAGAGATCTAGAGATTTGATATCTTC 430
Db 246 ATACACACCAATTCATACAAAAAGATTTGGCAGAGATCTAGAGATTTGATATCTTC 305
QY 431 CTAAAGTAAACGGTGAAGACCTTTGGGGGATGACGTCGTTGGCTAGCGGCGAGCAG 490
Db 306 CTAAAGTAAACGGTGAAGACCTTTGGGGGATGACGTCGTTGGCTAGCGGCGAGCAG 365
QY 491 ATTTCTTTGGCTCAATTTGGTCCAAAGCGGCTAACTTGACAGCATTAATACACTG 550
Db 366 ATTTCTTTGGCTCAATTTGGTCCAAAGCGGCTAACTTGACAGCATTAATACACTG 425
QY 551 ATGCTTAACCCGTAACCGTATCTAACCAAGATTCAT-----GATTAGCGCTAGC 601
Db 426 ATGCTTAACCCGTAACCGTATCTAACCAAGATTCATCGAAGCTCGTATTAGAGCTTAGC 485
QY 602 AACCAAAACCCACACATTTTATTGAGAGATCTAGAAAAAGTTAGGTGAACAACCTACTG 661
Db 486 AACCAAAACCCACACATTTTATTGAGAGATCTAGAAAAAGTTAGGTGAACAACCTACTG 545
QY 662 GTCATGTTCTTCAGTTTATGAAAGATTTGGTTCAGTTAGTCAAAAGTAAAAATATAGATA 721
Db 546 GTCATGTTCTTCAGTTTATGAAAGATTTGGTTCAGTTAGTCAAAAGTAAAAATATAGATA 605
QY 722 TTTCCATTAATATGATCCACAGAAAGATTTGGAGGTTTTTGGCATAAGATTAATAGC 781
Db 606 TTTCCATTAATATGATCCACAGAAAGATTTGGAGGTTTTTGGCATAAGATTAATAGC 665
QY 782 ATGATATCGAATTTGTCAGAAAGATTTCTAGCTTATTTTACCCGAGATACCATTTCTTA 841
Db 666 ATGATATCGAATTTGTCAGAAAGATTTCTAGCTTATTTTACCCGAGATACCATTTCTTA 725
QY 842 AAGCGGCTATTTATGCAACCAACCTGCAAAAGTGCAAGCAGATGTAAGAGATTCCTTG 901
Db 726 AAGCGGCTATTTATGCAACCAACCTGCAAAAGTGCAAGCAGATGTAAGAGATTCCTTG 785
QY 902 AATCATGCCGATATACACATGGGATTTGGCGGCTTACGAGATGATATTTCTCTT 961
Db 786 AATCATGCCGATATACACATGGGATTTGGCGGCTTACGAGATGATATTTCTCTT 845
QY 962 TAACCCGATGATGATGATGATATTTTGAAGATGATGTTGATTCATGATCATC 1021
Db 846 TAACCCGATGATGATGATGATATTTTGAAGATGATGTTGATTCATGATCATC 905
QY 1022 ATGATGATCCCGTAGCAAGTTGCGTGAAGAAATAGCTGAGCTTACCGCGGAATTAAGA 1081
Db 906 ATGATGATCCCGTAGCAAGTTGCGTGAAGAAATAGCTGAGCTTACCGCGGAATTAAGA 965
QY 1082 TTTATTCAGTTATTCAGCGGAATTAATATAGATCTGCTATAGTATGGCACATTAATA 1141
Db 966 TTTATTCAGTTATTCAGCGGAATTAATATAGATCTGCTATAGTATGGCACATTAATA 1025
QY 1142 TCCATGATTAATCATTAATCTGATGATTAATAATTTATATGTTATPACAGATGAAGAG 1201
Db 1026 TCCATGATTAATCATTAATCTGATGATTAATAATTTATATGTTATPACAGATGAAGAG 1085
QY 1202 TTTTAAAGCCAGCGAGAGTACAAAATTTCTGAGAAAATGCTTCAACACCATTCAG 1261
Db 1086 TTTTAAAGCCAGCGAGAGTACAAAATTTCTGAGAAAATGCTTCAACACCATTCAG 1145
QY 1262 TGGATGGAGCGGAGAAAATATAGTCTCGATTAAGAGACTTTCTTGAAGTGAAGATAAAA 1321
Db 1146 TGGATGGAGCGGAGAAAATATAGTCTCGATTAAGAGACTTTCTTGAAGTGAAGATAAAA 1205
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QY 1322 GAACGGGCGTTGGGTAATCTGAAAAACTCATACTTTATATAAGATAATAGAT 1381
Db 1206 GAACGGGCGTTGGGTAATCTGAAAAACTCATACTTTATATAAGATAATAGAT 1265
QY 1382 TATTCACCTTTCGCAACCACTGCTGGGATAAATCCAGCGCGCTCAACGATGTTAGCC 1441
Db 1266 TATTCACCTTTCGCAACCACTGCTGGGATAAATCCAGCGCGCTCAACGATGTTAGCC 1325
QY 1442 AAAAAACAACCTAGCTGTCGATATTACATCAGTTTATTCAGCTATTTGAAGCACTGA 1501
Db 1326 AAAAAACAACCTAGCTGTCGATATTACATCAGTTTATTCAGCTATTTGAAGCACTGA 1385
QY 1502 ACCGTTTCATGAGAAATATGATTCAGTATGATGATCAACGCTGCTAGATGACAGCTGTGA 1561
Db 1386 ACCGTTTCATGAGAAATATGATTCAGTATGATGATGATCAACGCTGCTAGATGACAGCTGTGA 1445
QY 1562 AATGA 1566
Db 1446 AATGA 1450

RESULT 3
T04222
AC T04222 standard; DNA; 1014 BP.
ID T04222;
AC T04222;
DT 18-APR-1996 (first entry)
DE Partial lcrV (V antigen) gene of Y. pestis.
KW lcrV; V antigen; virulence; plague; vaccine; epitope; ss.
OS Yersinia pestis.
FT cds location/Qualifiers
FT 1..990
FT /*tag= a
FT /note= "V antigen"
PD W09524475-A1.
PD 14-SEP-1995.
PF 06-MAR-1995; G00481.
PR 08-MAR-1994; GB-004577.
PA (MINA) UK SEC FOR DEFENCE.
PI Leary SEC, Tithall RW, Williamson ED, Leary SE;
DR WPT_95-328268/42.
DR P-PSDB: R/9961.
PT Recombinant DNA expressing Yersinia pestis V antigen - useful in
PT oral or parenteral vaccines for protection against plague
PS Claim 6; Page 11-13; 25pp; English.
CC T04222-23 are DNA sequences (lcrV) encoding all or a protective epitopic
CC part of the mature V protein of Yersinia pestis. The protein was
CC expressed as a fusion protein with maltose binding protein. Y. pestis is
CC glutathione-S-transferase in 3 different plasmid vectors.
CC the highly virulent causative organism of plague in a wide range of
CC animals, including man. The V antigen (lcrV) is an unstable 37.3 kDa
CC monomeric peptide encoded on the ca. 70 kb lcr plasmid. The V antigen
CC is postulated to act as a virulence antigen, and transformed
CC microorganisms conty. recombinant DNA encoding a V antigen protein/
CC peptide are useful in vaccines to protect against plague.
SO Sequence 1014 BP; 346 A; 181 C; 201 G; 286 T;

Query Match 62.4%; Score 976.8; DB 1; Length 1014;
Best Local Similarity 99.8%; Pred. No. 7.2e-251;
Matches 978; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 587 TGAATGAGCCCTACGAAACCAACCAACATTTATTTAGAGATCTAGAAAAAGTTAGGG 646
Db 11 TCATTAGAGCCCTACGAAACCAACCAACATTTATTTAGAGATCTAGAAAAAGTTAGGG 70
QY 647 TCGAACAACTCTGCTGCTGCTCTTCAAGTTTGAAGATTTGTTAGTCAAG 706
Db 71 TCGAACAACTCTGCTGCTGCTCTTCAAGTTTGAAGATTTGTTAGTCAAG 130
QY 707 ATPAAAAATATAGATATTTCCATTAATATATGATCCAGAAAAGATTGCGAGATTTTGCCA 766
Db 131 ATPAAAAATATAGATATTTCCATTAATATATGATCCAGAAAAGATTGCGAGATTTTGCCA 190
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Db 551 GTGCACCATTAATATCCATGATTAATTCATTATCTCATGATATAAAATTATATGCTT 610
Qy 1187 ATACAGATGAAGAGATTTTAAAGCCAGCCAGATACAAAATTCGAGAAATGCCCTC 1246
Db 611 ATACAGATGAAGAGATTTTAAAGCCAGCCAGATACAAAATTCGAGAAATGCCCTC 670
Qy 1247 AAACCACTTCAGGTGATGGAGGAGAGAAAAAATAGCTTCGATTAAGAGACTTCTTG 1306
Db 671 AAACCACTTCAGGTGATGGAGGAGAGAAAAAATAGCTTCGATTAAGAGACTTCTTG 730
Qy 1307 GAAGGAGATTAAGAACCGGGGGCTGGTATCTGAAAACATCATCTCTTATAA 1366
Db 731 GAAGGAGATTAAGAACCGGGGGCTGGTATCTGAAAACATCATCTCTTATAA 790
Qy 1367 AAGATAATTAATGATTAATCTACTTTGCCACCACTGCTCGGATTAAGTCCAGCGCTCA 1426
Db 791 AAGATAATTAATGATTAATCTACTTTGCCACCACTGCTCGGATTAAGTCCAGCGCTCA 850
Qy 1427 ACGACTTGGTTAGCCAAAACAACTCAGCTGCTGATTAATACATCAGCTTTAAATTCAG 1486
Db 851 ACGACTTGGTTAGCCAAAACAACTCAGCTGCTGATTAATACATCAGCTTTAAATTCAG 910
Qy 1487 CTATTGAAGCATGAACCGTTTCATTCAGAAATATGATTCAGTATGATGATGATGATG 1546
Db 911 CTATTGAAGCATGAACCGTTTCATTCAGAAATATGATTCAGTATGATGATGATGATG 970
Qy 1547 ATGACACGCTGCTGAATGA 1566
Db 971 ATGACACGCTGCTGAATGA 990

RESULT 5

T38243
ID T38243 standard; DNA: 1014 BP.
AC T38243: 1996 (first entry)
DE 28-DEC-1996 (first entry)
DE Y. pestis lcrV (V antigen) gene.
KW Plague vaccine; genetic immunisation; V antigen; lcrV;
KW FI antigen; ds.
OS Yersinia pestis strain GB.
FH Key
FH Location/Qualifiers
FT cds
FT 1. .990
FT /tag= a
FT misc_feature
FT 1. .10
FT /tag= b
FT /note= "vector pGEX-5X-2-derived bases"
FT 16
FT /tag= c
FT /note= "base 16 is altered to a C from an
FT A to create an EcoRI site"
FT 1006
FT /tag= d
FT /note= "base 1006 is altered to a T to create a
FT second in-frame stop codon"

PN M09628551-A1.
PD 19-SEP-1996.
PE 13-MAR-1996: G00571.
PR 13-MAR-1995: GB-005059.
PR 15-SEP-1995: GB-018946.
PR 05-DEC-1995: GB-024825.
PA (MIMA) UK SEC FOR DEFENCE.
PI Bennett AM, Leary SEC, Oyston PCF, Tiltball RM, Williamson ED;
DR WPI: 96-433824/43.
P-BSDB: W01041.
PT Yersinia pestis V antigen and FI antigen or their protective
PT epitopic parts - useful in vaccine for protection against plague
PS Claim 5: Page 32-35: 98BP: English.
CC A lcrV gene sequence (T38243) codes for the Yersinia pestis V
CC antigen (W01041) which is capable of evoking protective immune
CC responses in animals. The gene was amplified from Y. pestis
CC DNA by PCR using primers (T38251 and T38259) homologous to the 5'
CC and 3' ends of the gene. The gene was inserted into vector
CC pGEX-5x-2, pMAL-p2 or pMAL-c2 (see also T38242) to allow prodn. of

CC recombinant V antigen for use in vaccines against plague.
CC Expression in gut-colonising organisms and attenuated Salmonella
CC typhi allows live vaccine prodn. FI/V antigen fusions were also
CC created (see also T38249 and T38256). The gene can itself be used
CC in genetic vaccines.
SQ Sequence 1014 BP: 343 A: 184 C: 205 G: 282 T:

Query Match 62.2%; Score 974.8; DB 1: Length 1014;
Best Local Similarity 99.8%; Pred. No. 2.5e-250;
Matches 976; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 589 ATTAGAGCTTACGAAACCAACCAACATTTTATGAGATCTAGAAAAGTTAGGGTG 648
Db 13 ATTGAGCTTACGAAACCAACCAACATTTTATGAGATCTAGAAAAGTTAGGGTG 72
Qy 649 GAACAATTTACTGTCATGATGTTCTTCACTTTAGAGAATTTGTTCACTAGTCAAGAT 708
Db 73 GAACAATTTACTGTCATGATGTTCTTCACTTTAGAGAATTTGTTCACTAGTCAAGAT 132
Qy 709 AAAAATATAGATTTTCCATTAATATATGATCCAGAAAAGATTGGAGTTTTCCTAAT 768
Db 133 AAAAATATAGATTTTCCATTAATATATGATCCAGAAAAGATTGGAGTTTTCCTAAT 192
Qy 769 AGAGTAATTTACTGATGATATGATGATGCTCAAGAAAATCTAGTTATTTCTACCCGAG 828
Db 133 AGAGTAATTTACTGATGATATGATGATGCTCAAGAAAATCTAGTTATTTCTACCCGAG 252
Qy 829 GATACCAATTTTAAAGGGGCTATTATGACAAACCAACTGCAAAATGGCATCAAGGAGTA 888
Db 253 GATGCAATTTTAAAGGGGCTATTATGACAAACCAACTGCAAAATGGCATCAAGGAGTA 312
Qy 889 AAAGAGTTCTTGAATTCATCCGCCGATACACATATGGGAATTCGGGGCTTATGACAGTA 948
Db 313 AAAGAGTTCTTGAATTCATCCGCCGATACACATATGGGAATTCGGGGCTTATGACAGTA 372
Qy 949 ATGCAATTTCTCTTAAACCGCGCATGCTATGATGATGATTTTAAAGTATGTTGAT 1008
Db 373 ATGCAATTTCTCTTAAACCGCGCATGCTATGATGATGATTTTAAAGTATGTTGAT 432
Qy 1009 TCAATGAATCATCATGATGATGATCCCGTAGCAAGTTGCTGGAAGATTAAGTACCTTACC 1068
Db 433 TCAATGAATCATCATGATGATGATCCCGTAGCAAGTTGCTGGAAGATTAAGTACCTTACC 492
Qy 1069 GCGGAATTAAGATTTTATTCAGTTATTAAGCCGAAATTAATACATCTGCTGATGAT 1128
Db 493 GCGGAATTAAGATTTTATTCAGTTATTAAGCCGAAATTAATACATCTGCTGATGAT 552
Qy 1129 GGCACCATTAATATCATGATTAATCCATTAATCTCATGATGATTAATATATGATAT 1188
Db 553 GGCACCATTAATATCATGATTAATCCATTAATCTCATGATGATTAATATATGATAT 612
Qy 1189 ACAGATGAAGAGATTTTAAAGCCAGCCAGAGTACAAAATTTCTGAGAAAATGCCCTCAA 1248
Db 613 ACAGATGAAGAGATTTTAAAGCCAGCCAGAGTACAAAATTTCTGAGAAAATGCCCTCAA 672
Qy 1249 ACCACCATTCAGGTGATGATGAGGAGCAAAAAAATATGCTGATTAAGAGACTTTCTTGA 1308
Db 673 ACCACCATTCAGGTGATGATGAGGAGCAAAAAAATATGCTGATTAAGAGACTTTCTTGA 732
Qy 1309 AGTGAATTAAGAAACCGGGGGCTGGTAACTGAAAATCTACTCTTATAATAA 1368
Db 733 AGTGAATTAAGAAACCGGGGGCTGGTAACTGAAAATCTACTCTTATAATAA 792
Qy 1369 GATAATTAATGATTTTCTACTTTGCCACCACTCTCGATTAATCCAGCCGCTCAAC 1428
Db 793 GATAATTAATGATTTTCTACTTTGCCACCACTCTCGATTAATCCAGCCGCTCAAC 852
Qy 1429 GACTTGGTTAGCCAAAACAACTCAGCTGCTGATTAATTAATTAATTAATTAATTAAT 1488
Db 853 GACTTGGTTAGCCAAAACAACTCAGCTGCTGATTAATTAATTAATTAATTAATTAAT 912
Qy 1489 ATTGAAGCATGAACCGTTTCAATTAAGAAATATGATTAAGATGATCAACGCTGCTAAT 1548

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Db 913 ATTGAAGCAGCTGACCGTTTCATTGCAAAATATGATTCAGTATGCAAGCTGTGATGAT 972
OY 1549 GACACGCTCTGTGTAATGA 1566
|||||
Db 973 GACACGCTGTGTAATGA 990

RESULT 6
T04223
ID T04223 standard; DNA: 1014 BP.
AC T04223:
DT 18-APR-1996 (first entry)
DE Partial LcrV (V antigen) gene of Y. pestis.
KW LcrV; V antigen; virulence; plague; vaccine; epitope; ss.
OS Yersinia pestis.
FH Key Location/Qualifiers
FT cds 1..990
FT /tag= a
PN WO9524475-A1.
PD 14-SEP-1995.
PE 06-MAR-1995; G00481.
PR 08-MAR-1994; GB-004577.
PA (MINA) UK SEC FOR DEFENCE.
PI Leary SEC, Tibball RW, Williamson ED, Leary SE;
DR WPI: 95-328268/42.
P-PSDB: R79962.
PT Recombinant DNA expressing Yersinia pestis V antigen - useful in
PT oral or parenteral vaccines for protection against plague
PS Claim 6: Page 15-16: 25pp: English.
CC T04222-23 are DNA sequences (LcrV) encoding all or a protective epitopic
CC part of the mature V protein of Yersinia pestis. The protein was
CC expressed as a fusion protein with maltose binding protein or
CC glutathione-S-transferase in 3 different plasmid vectors. Y. pestis
CC is the highly virulent causative organism of plague in a wide range of
CC animals, including man. The V antigen (LcrV) is an unstable 37.3 kDa
CC monomeric peptide encoded on the ca. 70 kb Lcr plasmid. The V antigen
CC is postulated to act as a virulence antigen, and transformed
CC microorganisms contg. recombinant DNA encoding a V antigen protein/
CC peptide are useful in vaccines to protect against plague.
SQ Sequence 1014 BP; 343 A; 185 C; 204 G; 282 T;
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Query Match 62.1%; Score 973.2; DB 1; Length 1014;
Best Local Similarity 99.7%; Pred. No. 6.6e-250;
Matches 975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 589 ATTGAGCGCTAGCAACAAACCCACACATTTTATGAGATCTAGAAAAAGTTAGGCTG 648
|||||
Db 13 ATTGAGCGCTAGCAACAAACCCACACATTTTATGAGATCTAGAAAAAGTTAGGCTG 72
OY 649 GAACAACCTACTGTCATGGTCTTCAGTTTGAAGAATGGTTCAGTTAGTCAAGAAT 708
|||||
Db 73 GAACAACCTACTGTCATGGTCTTCAGTTTGAAGAATGGTTCAGTTAGTCAAGAAT 132
OY 709 AAAAATATGATATTTCCATTAAATATGATCCAGAAAAAGATTCGGAATTTGCCAAT 768
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Db 133 AAAAATATGATATTTCCATTAAATATGATCCAGAAAAAGATTCGGAATTTGCCAAT 192
OY 769 AGAGTAATTACTGATATGATATGATGCTCAAGAAATCCTACTATTATTTCACCCGAG 828
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Db 193 AGAGTAATTACTGATATGATATGATGCTCAAGAAATCCTACTATTATTTCACCCGAG 252
OY 829 GATACCATTTCTTAAAGCGGCTTATGACAACCACTGCAAAATGGATCAAGCAGATG 888
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Db 253 GATGCAATTTCTTAAAGCGGCTTATGACAACCACTGCAAAATGGATCAAGCAGATG 312
OY 889 AAAGAGTCTCTTGAATCATGCGGAATACCAATGGGAATTCGGCGCTTCATGGCAGTA 948
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Db 313 AAAGAGTCTCTTGAATCATGCGGAATACCAATGGGAATTCGGCGCTTCATGGCAGTA 372
OY 949 ATGCATTTCTCTTAAACCGCGGATGCTATGATGATGATTTTGAAGAAGATTTGAT 1008
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Db 373 ATGCATTTCTCTTAAACCGCGGATGCTATGATGATGATTTTGAAGTGAATGTTGAT 432
OY 1009 TCAATGAATCATGATGATGATGATGCGGTAGCAAGTTGCGTGAAGAATTTAGCTAGCTTACC 1068
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Db 433 TCATGAATCATGATGATGATGATGCGGTAGCAAGTTGCGTGAAGAATTTAGCTAGCTTACC 492
OY 1069 GCCGAATTAAGATTTTATTCAGTTATTCAGCCGGAATTAATAGCATCTGCTAGTACT 1128
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Db 493 GCCGAATTAAGATTTTATTCAGTTATTCAGCCGGAATTAATAGCATCTGCTAGTACT 552
OY 1129 GGCACCATTAATTCATGATTAATTCATTAATTCATGATGATGATGATGATGATGAT 1188
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Db 553 GGCACCATTAATTCATGATTAATTCATTAATTCATGATGATGATGATGATGATGAT 612
OY 1189 ACAGATGAAGAGATTTTAAAGCAGCAGCAGAGTACAAATTTCTCGAGAAATGCTCAA 1248
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Db 613 ACAGATGAAGAGATTTTAAAGCAGCAGCAGAGTACAAATTTCTCGAGAAATGCTCAA 672
OY 1249 ACCACCATTCAGTGTGATGGAGACGAGAAAAAATATGTTCTGATAAGACATTTCTTGA 1308
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Db 673 ACCACCATTCAGTGTGATGGAGACGAGAAAAAATATGTTCTGATAAGACATTTCTTGA 732
OY 1309 AGTGAATTAATGAATTAATTCATGTTGCGCACCATCTGCTGATTAAGTCAAGCTTATATA 1368
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Db 733 AGTGAATTAATGAATTAATTCATGTTGCGCACCATCTGCTGATTAAGTCAAGCTTATATA 792
OY 1369 GATTAATTAATGAATTAATTCATGTTGCGCACCATCTGCTGATTAAGTCAAGCTTATATA 1428
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Db 793 GATTAATTAATGAATTAATTCATGTTGCGCACCATCTGCTGATTAAGTCAAGCTTATATA 852
OY 1429 GACTTGTTAGCCAAACAACTACGCTGCTGATTAATTAATTAATTAATTAATTAAT 1488
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Db 853 GACTTGTTAGCCAAACAACTACGCTGCTGATTAATTAATTAATTAATTAATTAAT 912
OY 1489 ATTGAAGCAGCTGACCGTTCAATTCAGAAATATGATTCGATGCAAGCTGCTAGAT 1548
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Db 913 ATTGAAGCAGCTGACCGTTCAATTCAGAAATATGATTCGATGCAAGCTGCTAGAT 972
OY 1549 GACACGCTGTGTAATGA 1566
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Db 973 GACACGCTGTGTAATGA 990

RESULT 7
V41594
ID V41594 standard; DNA: 544 BP.
AC V41594:
DT 26-OCT-1998 (first entry)
DE Nucleotide sequence of FI antigen nYFI(a)sec544.
KW FI antigen; plasmid; vaccine; plague; ds.
OS Yersinia pestis.
FH Key Location/Qualifiers
FT cds 17..529
FT /tag= a
FT /product= "FI antigen"
PN WO9824912-A2.
PD 11-JUN-1998.
PE 04-DEC-1997; U22617.
PR 04-DEC-1996; US-767115.
PA (HESK-) HESKA CORP.
PI Hanes EJ, Osorio JE, Thomas RE;
DR WPI: 98-333331/29.
P-PSDB: W59782.
PT Protection of animals against plague - using nucleic acid encoding
PT antigen from Yersinia, Pasteurella and Francisella spp.
PS Claim 8: Page 51: 75pp; English.
CC This is the nucleotide sequence of a Yersinia pestis FI antigen, used
CC in the method of the invention. Plasmid and host cells are used to
CC produce recombinant antigens, especially Yersinia pestis antigens.
CC The recombinant antigens can be used in vaccines that are capable of
CC protecting an animal from contracting plague.
SQ Sequence 544 BP; 164 A; 120 C; 114 G; 146 T;
```

Query Match 33.0%; Score 517.2; DB 1; Length 544;
 Best Local Similarity 98.5%; Pred. No. 1.4e-128;
 Matches 522; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 68 ATATGAAAAAATCAGTCCGTTATGCCATTCGATTATTGGACATTCGAACTGCTTA 127
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 DB 15 ATATGAAAAAATCAGTCCGTTATGCCATTCGATTATTGGACATTCGAACTGCTTA 74

QY 128 ATCGGCGAGATTAACTGCAAGCACCCTGCAACGGCACTCTGTGAACCCGCCGA 187
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 DB 75 ATCGGCGAGATTAACTGCAAGCACCCTGCAACGGCACTCTGTGAACCCGCCGA 134

QY 188 TCACCTTACATATAAGGAAGCGCTCCAAATTAATATGACAAATGAAACATCGATA 247
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 DB 135 TCACCTTACATATAAGGAAGCGCTCCAAATTAATATGACAAATGAAACATCGATA 194

QY 248 CAGAAATTAATGTTGAGCTTACTCTTGGCGGCTATAAAGCAAGAACCTAGACAT 307
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 DB 195 CAGAAATTAATGTTGAGCTTACTCTTGGCGGCTATAAAGCAAGAACCTAGACAT 254

QY 308 CTGTACTTACATAGAGATCGCGGGGTATGCCATTAATTAATTAATTTCTAGAGATG 367
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 DB 255 CTGTACTTACATAGAGATCGCGGGGTATGCCATTAATTAATTAATTTCTAGAGATG 314

QY 368 GAATAACCAACCAATTCATCAAAAAGTATGCAAGATTTAGAGATTTGATATCT 427
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 DB 315 GAATAACCAACCAATTCATCAAAAAGTATGCAAGATTTAGAGATTTGATATCT 374

QY 428 CTCCTAAGTAAACGGTGAACCTTGTGGGGATGACGTCGTCCTAGCGGAGCC 487
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 DB 375 CTCCTAAGTAAACGGTGAACCTTGTGGGGATGACGTCGTCCTAGCGGAGCC 434

QY 488 AGGATTTCTTGTTCGTCATTTGTTCCAAAGCGGCTAACTTGCAAGCAATTAACA 547
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 DB 435 AGGATTTCTTGTTCGTCATTTGTTCCAAAGCGGCTAACTTGCAAGCAATTAACA 494

QY 548 CTGATGCTGAACCGTAAACCGTATCTAACCAAGATTCATGATTAAGCC 597
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 DB 495 CTGATGCTGAACCGTAAACCGTATCTAACCAAGATTCATGATTAAGCC 544

RESULT 8
 Q92819
 ID 092819 standard: DNA; 542 BP.
 AC 17-DEC-1995 (first entry)
 DE Yersinia pestis cafi (F1) antigen in plasmid pFOR1b.
 KW Vaccine; antigen; Salmonella typhimurium; Salmonella typhi;
 KM bubonic plague; pneumonic plague; ds.
 OS Yersinia pestis.
 FH key
 FT cds
 FT 2. .7
 FT /*tag= a
 FT /note= "first protein encoded by pFOR1b"
 FT 1. .6
 FT misc_feature
 FT /*tag= b
 FT 336. .541
 FT misc_feature
 FT /*tag= c
 FT /note= "cafi open reading frame downstream seq."
 FT 21. .530
 FT cds
 FT /*tag= d
 FT /note= "cafi fusion protein"
 PN MO9518231-A1.
 PD 06-JUL-1995.
 PF 23-DEC-1994; G02818.
 PR 24-DEC-1993; GB-026425.
 PA (MINA) UK SEC FOR DEFENCE.
 PI Howells A, Leary SEC, Oyston PCF, Tittball RW, Williamson ED;
 DR WPI; 95-246396/32.
 DR P-PSDB; R76528.
 PT DNA constructs capable of transforming microorganisms - which can be
 PT used as live or attenuated vaccines which induce an immune response,

PT against Yersinia pestis, at mucosal surfaces.
 PS Disclosure: Page 19-20; 27pp: English.
 CC The sequence represents the plasmid pFOR1b including the entire
 CC Y. pestis cafi (F1) antigen gene having a 5' tail including a SacI
 CC restriction site, and up to 7ATAG downstream of the cafi ORF.
 CC The DNA construct can be used to transform human or animal gut
 CC colonizing microorganisms, specifically attenuated Salmonella
 CC typhimurium or Salmonella typhi. The transformed microorganisms
 CC can be used as live/attenuated vaccines which induce immune
 CC responses at mucosal surfaces. The vaccines provide protection
 CC against infection with Y. pestis, and are parenterally and orally
 CC active vaccines offering protection against bubonic and pneumonic
 CC plague.
 SQ Sequence 542 BP; 164 A; 118 C; 114 G; 146 T;

Query Match 33.0%; Score 516.8; DB 1; Length 542;
 Best Local Similarity 99.6%; Pred. No. 1.8e-128;
 Matches 518; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 68 ATATGAAAAAATCAGTCCGTTATGCCATTCGATTATTGGACATTCGAACTGCTTA 127
 |||||||
 DB 19 ATATGAAAAAATCAGTCCGTTATGCCATTCGATTATTGGACATTCGAACTGCTTA 78

QY 128 ATCGGCGAGATTAACTGCAAGCACCCTGCAACGGCACTCTGTGAACCCGCCGA 187
 |||||||
 DB 79 ATCGGCGAGATTAACTGCAAGCACCCTGCAACGGCACTCTGTGTGAACCCGCCGA 138

QY 188 TCACCTTACATATAAGGAAGCGCTCCAAATTAATATGACAAATGAAACATCGATA 247
 |||||||
 DB 139 TCACCTTACATATAAGGAAGCGCTCCAAATTAATATGACAAATGAAACATCGATA 198

QY 248 CAGAAATTAATGTTGAGCTTACTCTTGGCGGCTATAAAGCAAGAACCTAGACAT 307
 |||||||
 DB 199 CAGAAATTAATGTTGAGCTTACTCTTGGCGGCTATAAAGCAAGAACCTAGACAT 258

QY 308 CTGTACTTACATAGAGATCGCGGGGTATGCCATTAATTAATTAATTTCTAGAGATG 367
 |||||||
 DB 259 CTGTACTTACATAGAGATCGCGGGGTATGCCATTAATTAATTAATTTCTAGAGATG 318

QY 368 GAATAACCAACCAATTCATCAAAAAGTATGCAAGATTTAGAGATTTGATATCT 427
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 DB 319 GAATAACCAACCAATTCATCAAAAAGTATGCAAGATTTAGAGATTTGATATCT 378

QY 428 CTCCTAAGTAAACGGTGAACCTTGTGGGGATGACGTCGTCCTAGCGGAGCC 487
 |||||||
 DB 379 CTCCTAAGTAAACGGTGAACCTTGTGGGGATGACGTCGTCCTAGCGGAGCC 438

QY 488 AGGATTTCTTGTTCGTCATTTGTTCCAAAGCGGCTAACTTGCAAGCAATTAACA 547
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 DB 439 AGGATTTCTTGTTCGTCATTTGTTCCAAAGCGGCTAACTTGCAAGCAATTAACA 498

QY 548 CTGATGCTGAACCGTAAACCGTATCTAACCAAGATTCATGATTAAGCC 587
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 DB 499 CTGATGCTGAACCGTAAACCGTATCTAACCAAGATTCATGATTAAGCC 538

RESULT 9
 T38248
 ID T38248 standard: DNA; 547 BP.
 AC T38248;
 DT 28-DEC-1996 (first entry)
 DE Y. pestis F1 antigen cafi gene (including signal sequence).
 KW Plaque; vaccine; genetic immunisation; F1 antigen; cafi;
 OS Yersinia pestis strain GB.
 FH key
 FT signal_peptide
 FT 29. .91
 FT /*tag= a
 FT mat_peptide
 FT 92. .538
 FT /*tag= b
 PN MO9628551-A1.
 PD 19-SEP-1996.

PF 23-DEC-1994: G02818.
 PR 24-DEC-1993: GB-026425.
 PA (MINA) UK SEC FOR DEFENCE.
 PI Howells A, Leary SEC, Oyston PCF, Tibball RW, Williamson ED;
 DR WPI: 95-246396/32.
 P-PSDB: R76526.
 DR DNA constructs capable of transforming microorganisms - which can be
 PT used as live or attenuated vaccines which induce an immune response,
 PT against Yersinia pestis, at mucosal surfaces.
 PS Claim 7: Page 15-16; 27pp; English.
 CC The sequence represents the plasmid pFGAL2a construct showing the
 CC fusion of the first few bases of beta-galactosidase in the vector
 CC with the Y. pestis cafI (FI) antigen minus its signal sequence and
 CC having a 5' tail including a SacI restriction site, and up to the
 CC cafI AACC-3' end with some vector bases. The DNA construct can be
 CC used to transform human or animal gut colonizing microorganisms,
 CC specifically attenuated Salmonella typhimurium or Salmonella typh.
 CC The transformed microorganisms can be used as live/attenuated
 CC vaccines which induce immune responses at mucosal surfaces. The
 CC vaccines provide protection against infection with Y. pestis, and
 CC are parenterally and orally active vaccines offering protection
 CC against bubonic and pneumonic plague.
 SQ Sequence 541 BP; 163 A; 120 C; 111 G; 147 T;

Query Match 28.9%; Score 452.2; DB 1; Length 541;
 Best Local Similarity 99.3%; Pred. No. 2.8e-111;
 Matches 454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 131 CGGCAGATTAACTGACAGACCACTGCAACGCACTCTGTTGAACGCCGATCA 190
 DB 6 CGGCAGATTAACTGACAGACCACTGCAACGCACTCTGTTGAACGCCGATCA 65
 QY 191 CTCTACATTAAGAAGGCGCTCAATTACAAATTATGACAATGAAACATGCATCAG 250
 DB 66 CTATTCATTAAGAAGGCGCTCAATTACAAATTATGACAATGAAACATGCATCAG 125
 QY 251 AATTACTGTTGGTACGCTTACTCTTGGCGGTATAAAACAGAACCATGACATCTG 310
 DB 126 AATTACTGTTGGTACGCTTACTCTTGGCGGTATAAAACAGAACCATGACATCTG 185
 QY 311 TTAACTTTAGATGCGCGGGGATGCCATGACTTAACTTACTCTCAGATGAA 370
 DB 186 TTAACTTTAGATGCGCGGGGATGCCATGACTTAACTTACTCTCAGATGAA 245
 QY 371 ATAACCAACCAATTCACATAAAGATGTTGGCAAGATCTAGAGATTGATCTCTC 430
 DB 246 ATAACCAACCAATTCACATAAAGATGTTGGCAAGATCTAGAGATTGATCTCTC 305
 QY 431 CTAAGTAAAGGTTGAGAACCTTGTGGGGATGACGTGCTTGGCTACGGGACGAG 490
 DB 306 CTAAGTAAAGGTTGAGAACCTTGTGGGGATGACGTGCTTGGCTACGGGACGAG 365
 QY 491 ATTCTTTGTCGCTCAATTGTTCCAAAGCGGTAACTTGACAGCGTAATACCTG 550
 DB 366 ATTCTTTGTCGCTCAATTGTTCCAAAGCGGTAACTTGACAGCGTAATACCTG 425
 QY 551 ATGCTGAACCGTACCGTATCTAACCAAGATTTCAT 587
 DB 426 ATGCTGAACCGTACCGTATCTAACCAATATTCAT 462

RESULT 14
 ID T38244
 AC T38244; standard: DNA; 541 BP.
 DT 28-DEC-1996 (first entry)
 DE Y. pestis cafI (FI antigen) gene.
 KW Plaque: vaccine; genetic immunisation; FI antigen; cafI;
 OS Yersinia pestis strain GB
 FH key misc_recomb Location/Qualifiers
 FT misc_recomb 1..6

FT FT /*tag= a
 FT FT /note="Includes the first few bases of the
 FT FT beta-galactosidase sequence in vector
 FT FT pFGAL2a"
 FT cds 2..457
 FT FT /*tag= b
 FT FT /product= mature FI antigen
 FT FT 536..541
 FT FT /*tag= c
 PN W09628551-A1.
 PD 19-SEP-1996.
 PR 13-MAR-1995: G00571.
 PR 13-MAR-1995: GB-005059.
 PR 15-SEP-1995: GB-018946.
 PR 05-DEC-1995: GB-024825.
 PA (MINA) UK SEC FOR DEFENCE.
 PI Bennett AM, Leary SEC, Oyston PCF, Tibball RW, Williamson ED;
 DR WPI: 96-433824/43.
 P-PSDB: W01042.
 DR Yersinia pestis V antigen and FI antigen or their protective
 PT epitopic parts - useful in vaccine for protection against plague
 PS Claim 7: Page 43-45; 98pp; English.
 CC The cafI gene (T38244) codes for the Yersinia pestis FI antigen
 CC (W01042), which is capable of evoking protective immune responses
 CC in animals. The gene was amplified from Y. pestis DNA by PCR using
 CC primers (T38245-46) homologous to the 5' and 3' ends of the gene.
 CC The cafI PCR product was ligated into pUC18 and transformed into E.
 CC coli JM109 to produce vector pFGAL2a. The cafI gene can be used to
 CC produce recombinant FI antigen for use in vaccines against plague.
 CC Expression in gut-colonising organisms and attenuated Salmonella
 CC typh allows prodn. of live vaccines. The gene can itself be used
 CC in genetic vaccines. FI/V antigen fusions were also created (see
 CC also T38249 and T38256).
 SQ Sequence 541 BP; 163 A; 120 C; 111 G; 147 T;

Query Match 28.9%; Score 452.2; DB 1; Length 541;
 Best Local Similarity 99.3%; Pred. No. 2.8e-111;
 Matches 454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 131 CGGCAGATTAACTGACAGACCACTGCAACGCACTCTGTTGAACGCCGATCA 190
 DB 6 CGGCAGATTAACTGACAGACCACTGCAACGCACTCTGTTGAACGCCGATCA 65
 QY 191 CTCTACATTAAGAAGGCGCTCAATTACAAATTATGACAATGAAACATGCATCAG 250
 DB 66 CTATTCATTAAGAAGGCGCTCAATTACAAATTATGACAATGAAACATGCATCAG 125
 QY 251 AATTACTGTTGGTACGCTTACTCTTGGCGGTATAAAACAGAACCATGACATCTG 310
 DB 126 AATTACTGTTGGTACGCTTACTCTTGGCGGTATAAAACAGAACCATGACATCTG 185
 QY 311 TTAACTTTAGATGCGCGGGGATGCCATGACTTAACTTACTCTCAGATGAA 370
 DB 186 TTAACTTTAGATGCGCGGGGATGCCATGACTTAACTTACTCTCAGATGAA 245
 QY 371 ATAACCAACCAATTCACATAAAGATGTTGGCAAGATCTAGAGATTGATCTCTC 430
 DB 246 ATAACCAACCAATTCACATAAAGATGTTGGCAAGATCTAGAGATTGATCTCTC 305
 QY 431 CTAAGTAAAGGTTGAGAACCTTGTGGGGATGACGTGCTTGGCTACGGGACGAG 490
 DB 306 CTAAGTAAAGGTTGAGAACCTTGTGGGGATGACGTGCTTGGCTACGGGACGAG 365
 QY 491 ATTCTTTGTCGCTCAATTGTTCCAAAGCGGTAACTTGACAGCGTAATACCTG 550
 DB 366 ATTCTTTGTCGCTCAATTGTTCCAAAGCGGTAACTTGACAGCGTAATACCTG 425
 QY 551 ATGCTGAACCGTACCGTATCTAACCAAGATTTCAT 587
 DB 426 ATGCTGAACCGTACCGTATCTAACCAATATTCAT 462

RESULT 15

092818

ID 092818 standard: DNA; 542 BP.

AC 092818;

DE Yersinia pestis caf1 (F1) antigen in plasmid pF51G3a.

KW vaccine; antigen; Salmonella typhimurium; Salmonella typhi;

OS Yersinia pestis.

FT Key Location/Qualifiers

FT cds 3..455

FT misc-feature 1..6

FT misc-feature 1..6

FT misc-feature 536..541

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Job time: 2661 sec

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QY 549 TGATGCTGTAACCGGTAAACGTAATCAACCAAGATTCAT 587
DB 425 TGATGCTGTAACCGGTAAACGTAATCAACCAAGATTCAT 463

Query Match 28.88; Score 451; DB 1; Length 542;
Best Local Similarity 98.98; Pred. No. 5.9e-111;
Matches 454; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 129 TGGCGCAGATTACTGACGACACTGCAAGCACTGTTGTAACGAGCCGCAT 188
DB 5 TCCCGCAGATTACTGACGACACTGCAAGCACTGTTGTAACGAGCCGCAT 64
QY 189 CACTTACATATAAGGAGCGCTCCCAATTACATATGAGACATGAAACATCATAC 248
DB 65 CACTTACATATAAGGAGCGCTCCCAATTACATATGAGACATGAAACATCATAC 124
QY 249 AGAATTAATGTTGTTGCTTACTCTTGGCGGTATATAAGGAGACCACTACACATC 308
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QY 309 TGTAACTTACAGATCCCGGGGTATCCCATGTACTTAACATTTTCTCTCAGATGG 368
DB 185 TGTAACTTACAGATCCCGGGGTATCCCATGTACTTAACATTTTCTCTCAGATGG 244
QY 369 AAATAACCAATTCCTACTCAAAAGTATGGCAAGATTCAGAGATTTTGTATCTC 428
DB 245 AAATAACCAATTCCTACTCAAAAGTATGGCAAGATTCAGAGATTTTGTATCTC 304
QY 429 TCGTAAGTAAAGGAGTGAACCTTGTGGGGGATGACGTCGCTTGCTACGGGACCA 488
DB 305 TCGTAAGTAAAGGAGTGAACCTTGTGGGGGATGACGTCGCTTGCTACGGGACCA 364

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Percent Similarity: 100.000 Percent Identity: 94.444

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seq_documentation_block:

Sequence 25, Application US/08405496A

Patent No. 5919665

GENERAL INFORMATION:

APPLICANT: WILLIAMS, JAMES A.

TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/405,496A

FILING DATE: 16-MAR-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/329,154

FILING DATE: 25-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/161,907

FILING DATE: 02-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/985,321

FILING DATE: 04-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/429,791

FILING DATE: 31-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: INGOLIA, DIANE E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: OPHD-01308

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1402 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1386

US-08-405-496A-25

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Percent Similarity: 100.000

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Percent Identity: 94.444

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seq_documentation_block:

Sequence 1, Application US/08332766A

Patent No. 5843647

GENERAL INFORMATION:

APPLICANT: JEFFREYS, Alec J.

TITLE OF INVENTION: SIMPLE TANDEM REPEATS

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESSES:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,766A

FILING DATE: 01-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9326052.9

FILING DATE: 21-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: BIRD, Donald J.

REGISTRATION NUMBER: 25,323

REFERENCE/DOCKET NUMBER: 217211/94/0434/GB

TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 377 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-332-766A-1

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Quality: 69.00

Ratio: 4.059

Percent Similarity: 85.000

Length: 20

Gaps: 0

Percent Identity: 55.000

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37 NNNNNNNHNCYOEDEK 18

seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-600-783-15

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seq_documentation_block:
; Sequence 15, Application US/08600783
; Patent No. 5962267
; GENERAL INFORMATION:
; APPLICANT: SHIN, Hang Cheol
; APPLICANT: CHANG, Seung Gu
; APPLICANT: KIM, Chong Suh1
; TITLE OF INVENTION: Proinsulin Derivative and Process
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHIN, Hang Cheol
; STREET: Saengma-Hanshin Apt. 102-1206,
; STREET: #245 Cholsan-dong
; CITY: Kwangmyung-shi
; STATE: Kyungki-do
; COUNTRY: Republic of Korea
; ZIP: 423-030
; ADDRESSEE: CHANG, Seung Gu
; STREET: Hyundai Apt. 71-203, Apkujong-dong,
; STREET: Kangnam-ku
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; ADDRESSEE: KIM, Dae Young
; STREET: Sosa Jukong Apt. 108-202, Sosa Bon-dong,
; STREET: Sosa-ku
; CITY: Bucheon-shi
; STATE: Kyungki-do
; COUNTRY: Republic of Korea
; ZIP: 422-230
; ADDRESSEE: KIM, Chong Suh1
; STREET: Garden Heights Apt. 202-801, #100,
; STREET: Hwangkeum-dong, Soosung-ku
; CITY: Taegu
; STATE: Taegu
; COUNTRY: Republic of Korea
; ZIP: 706-040
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk, 3.5 inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,783
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-2751
; FILING DATE: 15-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Shahan Islam
; REGISTRATION NUMBER: 32,507
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-1000
; TELEFAX: (212) 953-7249
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer DNA
; ANTI-SENSE: no
; US-08-600-783-15

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alignment_scores:
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Ratio: 5.636       Gaps: 0

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Percent Similarity: 100.000   Percent Identity: 100.000
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US-08-699-716a-2 x US-08-600-783-15 (1)
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3 HHHHHHHHNS 13
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5 HHHHHHHHNS 15
seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-068-747-8
seq_documentation_block:
; Sequence 8, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millita Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
; US-08-068-747-8

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alignment_scores:
Quality: 60.00      Length: 10
Ratio: 6.000       Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

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alignment_block:
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Align seg 1/1 to reverse of: US-08-068-747-8 from: 1 to: 36

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11 HHHHHHHH 2

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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-563-864-1

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seq_documentation_block:
; Sequence 1, Application US/08563864
; Patent No. 5674687
; GENERAL INFORMATION:
; APPLICANT: Hershfield, Bennett
; TITLE OF INVENTION: A METHOD FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: NUCLEIC ACID SAMPLES FROM DNA-CONTAINING ORGANISMS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/563,864
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,395
; FILING DATE: 31-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman Esq., Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/160 (D-1452)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-563-864-1

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; Quality: 60.00 Length: 10
; Ratio: 6.000 Gaps: 0
; Percent Similarity: 100.000 Percent Identity: 100.000

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3 HNNNNNNNN 12
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2 HNNNNNNNN 11

seq_name: /cgn2_6/ptodata/1/ina/PCTUS9_COMB.seq:PCT-US95-06839-1

seq_documentation_block:
; Sequence 1, Application PC/TUS9506839
; GENERAL INFORMATION:
; APPLICANT: Hershfield, Bennett
; TITLE OF INVENTION: A METHOD FOR THE IDENTIFICATION
; TITLE OF INVENTION: OF NUCLEIC ACID SAMPLES FROM DNA-CONTAINING ORGANISMS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
```

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STATE: New York
COUNTRY: USA
ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06839
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,395
; FILING DATE: 31-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman Esq., Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/160 (D-1452)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US95-06839-1

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; Quality: 60.00 Length: 10
; Ratio: 6.000 Gaps: 0
; Percent Similarity: 100.000 Percent Identity: 100.000

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Align seg 1/1 to: PCT-US95-06839-1 from: 1 to: 38
3 HNNNNNNNN 12
| | | | | | | |
2 HNNNNNNNN 11

seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-07-781-034-4

seq_documentation_block:
; Sequence 4, Application US/07781034
; Patent No. 5442050
; GENERAL INFORMATION:
; APPLICANT: Fishman, Jay A.
; TITLE OF INVENTION: Molecular Cloning of Antigens Shared By
; TITLE OF INVENTION: Rat- and Human-Derived Pneumocystis Carinii
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/781,034
; FILING DATE: 19911018
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; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
;   NAME: Granahan, Patricia
;   REGISTRATION NUMBER: 32,227
;   REFERENCE/DOCKET NUMBER: MGH91-02A
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617) 861-6240
;     TELEFAX: (617) 861-9540
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1189 base pairs
;       TYPE: NUCLEIC ACID
;       STRANDEDNESS: double
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA to mRNA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;   US-07-781-034-4

alignment_scores:
  Quality: 70.00      Length: 15
  Ratio: 5.385      Gaps: 0
  Percent Similarity: 86.667      Percent Identity: 80.000

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  203 HNNNNNNHHSSHT 189

seq_name: /cgn2_6/prodata/1/lna/PCTUS9_COMB.seq:PCT-US92-08328-4

seq_documentation_block:
; Sequence 4, Application PC/TUS9208328
; GENERAL INFORMATION:
;   APPLICANT: Fishman, Jay A.
;   TITLE OF INVENTION: Molecular Cloning of Antigens Shared By
;   TITLE OF INVENTION: Rat- and Human-Derived Pneumocystis Carinii
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;     STREET: Two Millita Drive
;     CITY: Lexington
;     STATE: Massachusetts
;     COUNTRY: USA
;     ZIP: 02173
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US92/08328
;     FILING DATE: 19920930
;   CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/781,034
;       FILING DATE: 18-OCT-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/768,166
;       FILING DATE: 30-SEP-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Granahan, Patricia
;     REGISTRATION NUMBER: 32,227
;     REFERENCE/DOCKET NUMBER: MGH91-02AA PCT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (617) 861-6240
;       TELEFAX: (617) 861-9540
;       TELEX: 951794
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; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1189 base pairs
;     TYPE: NUCLEIC ACID
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA to mRNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   PCT-US92-08328-4

alignment_scores:
  Quality: 70.00      Length: 15
  Ratio: 5.385      Gaps: 0
  Percent Similarity: 86.667      Percent Identity: 80.000

alignment_block:
  US-08-699-716A-2 x PCT-US92-08328-4/rev (4)  ..

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  |||||
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seq_documentation_block:
; Sequence 1, Application US/08332766A
; Patent No. 5843647
; GENERAL INFORMATION:
;   APPLICANT: JEFFREYS, Alec J.
;   TITLE OF INVENTION: SIMPLE TANDEM REPEATS
;   NUMBER OF SEQUENCES: 125
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
;     STREET: 1100 New York Avenue, N.W.
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20005-3918
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     OPERATING SYSTEM: IBM PC compatible
;     SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/332,766A
;     FILING DATE: 01-NOV-1994
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: GB 9326052.9
;     FILING DATE: 21-DEC-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: BIRD, Donald J.
;     REGISTRATION NUMBER: 25,323
;     REFERENCE/DOCKET NUMBER: 217211/M94/0434/CB
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (202) 861-3000
;       TELEFAX: (202) 822-0944
;       TELEX: 6714627 CUSH
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 377 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;     US-08-332-766A-1
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US-08-699-716A-2 x US-08-332-766A-30/rev (6)

APPLICANT: Gilbert-Rothst

TELEFAX: (216) 241-0816
 TELEX: 980499
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 941 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 33..941
 PCT-US95-01882A-3

alignment_scores:
 Quality: 64.00 Length: 11
 Ratio: 5.818 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-699-716A-2 x PCT-US95-01882A-3 (3)

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2 GHHHHHHHHH 12
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 77 GHHHHHHHHH 87

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 27, 1999, 17:36:42 ; Search time 27.29 Seconds
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Title: US-08-699-716a-1

Perfect score: 1566
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Scoring table:

Searched: 195662 seqs, 52875861 residues

Database :

Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5C.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5D.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCITUS9.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Dackfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53.4	3.4	1402	2	US-08-480-604A-25	Sequence 25, Appl
2	53.4	3.4	1402	4	US-08-405-496A-25	Sequence 25, Appl
3	48	3.1	7218	2	US-08-232-463-14	Sequence 14, Appl
4	39	2.5	4435	2	US-08-308-872B-5	Sequence 5, Appl
5	37.4	2.4	4365	5	PCT-US91-08525-31	Sequence 31, Appl
6	37.4	2.4	4365	5	PCT-US93-04384-11	Sequence 11, Appl
7	35	2.2	47	4	US-08-600-783-15	Sequence 15, Appl
8	34.8	2.2	2415	4	US-08-785-428-1	Sequence 1, Appl
9	34.8	2.2	1446	4	US-08-560-007B-4	Sequence 4, Appl
10	34.6	2.2	1100	3	US-08-179-557-20	Sequence 20, Appl
11	34	2.2	867	4	US-09-036-582-36	Sequence 36, Appl
12	33.2	2.1	10564	1	US-08-206-176-5	Sequence 5, Appl
13	33.2	2.1	9636	2	US-08-323-170B-1	Sequence 1, Appl
14	33	2.1	1888	2	US-08-229-145-13	Sequence 13, Appl
15	33	2.1	8920	3	US-08-446-855A-1	Sequence 1, Appl
16	33	2.1	2993	4	US-08-415-593-42	Sequence 42, Appl
17	32.8	2.1	891	3	US-07-941-523-19	Sequence 19, Appl
18	32.8	2.1	1959	3	US-08-137-175A-1	Sequence 1, Appl
19	32.8	2.1	2369	4	US-08-525-742-1	Sequence 6, Appl
20	32.6	2.1	3311	1	US-07-777-715-6	Sequence 8, Appl
21	32.6	2.1	3229	1	US-07-777-715-8	Sequence 8, Appl
22	32.6	2.1	2794	1	US-07-960-932-1	Sequence 1, Appl
23	32.6	2.1	2838	1	US-07-960-932-8	Sequence 8, Appl
24	32.6	2.1	2817	1	US-07-960-932-9	Sequence 9, Appl
25	32.6	2.1	2861	1	US-07-960-932-10	Sequence 10, Appl
26	32.6	2.1	2794	1	US-07-908-253-1	Sequence 1, Appl
27	32.6	2.1	3311	1	US-08-170-126-1	Sequence 3, Appl
28	32.6	2.1	3329	1	US-08-170-126-3	Sequence 9, Appl
29	32.6	2.1	2794	2	US-08-455-970A-1	Sequence 1, Appl
30	32.6	2.1	2838	2	US-08-455-970A-9	Sequence 9, Appl
31	32.6	2.1	2817	2	US-08-455-970A-11	Sequence 11, Appl
32	32.6	2.1	2861	2	US-08-455-970A-13	Sequence 13, Appl
33	32.6	2.1	2794	2	US-08-387-156-5	Sequence 5, Appl
34	32.6	2.1	2934	2	US-08-387-156-7	Sequence 7, Appl
35	32.6	2.1	2794	3	US-08-694-865-5	Sequence 5, Appl
36	32.6	2.1	2934	3	US-08-694-865-7	Sequence 7, Appl
37	32.6	2.1	2653	3	US-08-589-711-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-08-480-604A-25
; Sequence 25, Application US/08480604A
; Patent No. 5736139
; GENERAL INFORMATION:
; APPLICANT: KINK, JOHN A.
; APPLICANT: THALEY, BROCE S.
; APPLICANT: PADHYE, NISHA V.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
; PREVENTION OF C. DIFFICILE DISEASE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,604A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/422,711
; FILING DATE: 14-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/405,496
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,154
; FILING DATE: 25-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,907
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,321
; FILING DATE: 04-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/429,791
; FILING DATE: 31-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: INGOLIA, DIANE E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: OPMD-01763
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1402 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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Db 877 ACAATTATCATGATTAAGTTCACCTTGCTCCCAATAATTTATCTATTATCTATT 818
QY 1195 GAAGAGATTTTAAAGCCAGCGAGATACAAATTTCTCGAGAAAATGCCCTCAACACC 1254
Db 817 GTTTTTCATTTTAAGATTTGATTAATAACAAAACGACAAATAGTAATATCATC 758
QY 1255 ATTCAGGTGATGGAGCGAGA 1276
Db 757 ATGAACCTTAATGACCGAGATA 736

RESULT 10
US-08-179-557-20
Sequence 20, Application US/08179557
Patent No. 5837509
GENERAL INFORMATION:
APPLICANT: ISRAELSEN, Hans
APPLICANT: BECH HANSEN, Egon
APPLICANT: MADSEN, Soeren Michael
APPLICANT: JOHANSEN, Eric
APPLICANT: NILSSON, Dan
APPLICANT: VRANG, Astrid
TITLE OF INVENTION: Recombinant Lactic Acid Bacterium
TITLE OF INVENTION: Containing an inserted Promoter and Method of Constructing
NUMBER OF INVENTION: Same
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,557
FILING DATE: 07-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1579/92
FILING DATE: 30-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0988/93
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK94/00004
FILING DATE: 03-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,681
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30307/140/PLVI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..57
US-08-179-557-20

Query Match 2.2%; Score 34.6; DB 3: Length 1100;
Best Local Similarity 48.7%; Pred. No. 0.87;
Matches 94; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 607 AACCCACAACATTTTATGAGATCTAGAAAAGTTAGGCTGGAACAACACTACTGTCAT 666
Db 10 AAACCCAGAGAAAATAAGAAAAATCAGAAAGTCAAAACCCGAAATAGGCTGTTTTCT 69
QY 667 GGTCTTCAGTTTGAAGAATTGGTTCAGTTAGTCAAGATAAAATATAGATATTCC 726
Db 70 TTTTATATGTTTAGATAGTAGTCTAGTTATTTCTTGACAAAAATATATTGAT 129
QY 727 ATTAATATGATCCAGAAAAGATTGGAGGTTTTCGCCAATAGATAATGATGAT 786
Db 130 ATAAATTAATAGTTGCTGTTGAGACGACGTCTTCTTATATTCATCTAAATATTAT 189
QY 787 ATCGAATTGCCTCA 799
Db 190 TTGAAAAAGATTA 202

RESULT 11
US-09-036-582-36
Sequence 36, Application US/09036582A
Patent No. 5965381
GENERAL INFORMATION:
APPLICANT: van der Bruggen, Pierre
APPLICANT: Cornelis, Guy R.
TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS
TITLE OF INVENTION: WITH RECOMBINANT YERSINIA
FILE REFERENCE: 11154
CURRENT APPLICATION NUMBER: US/09/036,582A
CURRENT FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
LENGTH: 867
TYPE: DNA
ORGANISM: Yersinia enterocolitica
US-09-036-582-36

Query Match 2.2%; Score 34; DB 4: Length 867;
Best Local Similarity 44.3%; Pred. No. 1.1;
Matches 139; Conservative 0; Mismatches 175; Indels 0; Gaps 0;
QY 1010 CAATGATCATCATGATGATGCCCGTAGCAAGTTGCTGAAGATTAGCTGAGCTTACCG 1069
Db 539 caaaaaactttacaccgagagagatagcctgttgaataatcatgaagataataaag 598
QY 1070 CCGAATTAAGATTTATTCAGTTATTCAGCCGAAATTAATTAAGCATCTGTAGTAGTG 1129
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QY 1130 GCACCATTAATTCATGATTAATTCATTATCTCATGATGAATAAAATTTATGTTATA 1189
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QY 1190 CAGATGAAGATTTTAAAGCCAGCGCAGAGTACAAAATTTTCGAGAAAATGCTTAAA 1249
Db 719 cgcgggagttgtactgtttaaacaataaaatgaacacatttaataagtttgata 778
QY 1250 CCACCATTCAGGTGATGGAGCGAGAAAATAATAGTCGATTAAGATTTCTTGAA 1309
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QY 1310 GTGAGATTAAGA 1323
Db 839 ctgaataataaaca 852

RESULT 12

US-08-206-176-5
Sequence 5, Application US/08206176
Patent No. 5639940
GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Dairymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206.176
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
IMMEDIATE SOURCE:
FEATURE:
CLONE: human fibrinogen gamma chain
NAME/KEY: CDS
LOCATION: John(1799..1876, 1973..2017, 2207..2390, 2510
LOCATION: ..2603, 4211..4341, 4645..4778, 5758..5942, 7426
LOCATION: ..7703, 9342..9571)
US-08-206-176-5

Query Match 2.1% Score 33.2; DB 1; Length 10564;
Best Local Similarity 51.3%; Pred. No. 7.3;
Matches 77: Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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QY 748 GATTGGAGGTTTTCACATAGAGTAATTTACTGATGATATGGAATTGCTCAAGAAATC 807
DB 4056 TAAATTTACATTTTCCTCAAGAAAGAAATATTTATTCAGAAAGCACTCTTAAGAAATA 4115
QY 808 CTAGCTATTTTCTACCCGAGATACCAT 837
DB 4116 CTTACGAGTTTCCAAAGAAATATTAAT 4145

RESULT 13
US-08-323-170B-1
Sequence 1, Application US/08323170B
Patent No. 5733772
GENERAL INFORMATION:

APPLICANT: Williamson, Kim C.
APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmidum
TITLE OF INVENTION: flicliparum Transmission-Blocking Target Antigen, Pf5230
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor.
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323.170B
FILING DATE: 13-OCT-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,409
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Quine, Jonathan A.
REGISTRATION NUMBER: P-41,261
REFERENCE/DOCKET NUMBER: 015280-113100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 149..9556
US-08-323-170B-1

Query Match 2.1% Score 33.2; DB 2; Length 9636;
Best Local Similarity 52.1%; Pred. No. 6.9;
Matches 74: Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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DB 7139 TTTAAATAATCATTTATTTACAGCATATCTTAAGTACAGATACCTTTAATTTATTT 7198
QY 343 TACTTAACATTTACTTCTCAGAGATGAATAACACCAATTCATCAACAAAGTATGGC 402
DB 7199 AACTTCATGTAATTTGTTAATATCCAGAAACATGATATGTAATGATATGCAATTTGAG 7258
QY 403 AAGGATCTAGAGATTTGATTA 424
DB 7259 TCTGATTAATCGAAATTTGATA 7280

RESULT 14
US-08-229-145-13
Sequence 13, Application US/08229145
Patent No. 5691461
GENERAL INFORMATION:
APPLICANT: Hoke, Glenn D.
APPLICANT: Ecker, David J.
TITLE OF INVENTION: INHIBITION OF CANDIDA USING
TITLE OF INVENTION: OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Macklewitz &

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205 GHGSSVLEELVOLVKDKNIDISIKIDPRKDSYFANRVITDIELLKTL 254
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seq_documentation_block:
LOCUS A56808 1462 bp DNA PAT 03-MAR-1998
DEFINITION Sequence 16 from Patent WO9628551.
ACCESSION A56808
NID g3712821
VERSION A56808.1 GI:3712821
KEYWORDS
SOURCE Yersinia pestis.
ORGANISM Yersinia pestis
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE 1 (bases 1 to 1462)
AUTHORS Tlball,R.W., Williamson,E.D., Leary, Sophie,E.C., Oyston,P.C.,
Bennett and Alice,M.
TITLE VACCINES FOR PLAGUE
JOURNAL Patent: WO 9628551-A 16 19-SEP-1996;
SECR DEFENCE (GB)
COMMENT Other publication ZA 9602036 960716
Other publication AU 4951196 961002.
FEATURES
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HFS/LADRIDDDLKVIYDSNMHNGDARSKLREELAEELAEELAEELAEELAEELAE
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Ratio: 4.262 Gaps: 1
Percent Similarity: 98.963 Percent Identity: 98.340
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51 GGYKGTSTSVNFTDAAGDPMTLFTSQDGNHOFHTTVIGGSDSPDIS 100
143 SPKVENGLVGDVVLATGSODFEVRSIGSGKGLAAGKYDAYTVVSN 192
101 SPKVENGLVGDVVLATGSODFEVRSIGSGKGLAAGKYDAYTVVSN 150
193 Q...EFMIRAYEQNPQHFIEDEKRVBOLTHGSSVLEELVOLVKDKNI 239
151 QGIEGRIRAYEQNPQHFIEDEKRVBOLTHGSSVLEELVOLVKDKNI 200
240 DISIKYDPRKDSYFANRVITDIELLKILAEFLPEDALIKGGHYDNOL 289
201 DISIKYDPRKDSYFANRVITDIELLKILAEFLPEDALIKGGHYDNOL 250
290 QNGIKRYKEFLLESSPNTOMELRAFMAVHFS/LTADRIDDDLKVIYDSMN 339
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351 DKNLYGTTDEIFKASAEYKILEKMPQTTIOVDGSEKKIYISIKDPLSEN 400
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401 KRTGALGNLKNYSYNKDNNELSHFATTCSDKSRPLNDLVSOQKTOLSDI 450
490 TSRFNSAIEALNRFIOKYSVMORLLDDTSGK 521
451 TSRFNSAIEALNRFIOKYSVMORLLDDTSGK 482
seq_name: gb_pat:YEPICR
seq_documentation_block:
LOCUS YEPICR 2100 bp DNA BCT 26-APR-1993
DEFINITION Yersinia pestis lcrG, lcrV, and lcrH genes, complete cds.
ACCESSION M26405
NID g155448
VERSION M26405.1 GI:155448
KEYWORDS lcrG protein; lcrH protein; lcrV protein; V antigen.
SOURCE 75kb virulence plasmid.
ORGANISM Yersinia pestis
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE 1 (bases 1 to 2100)
AUTHORS Price,S.B., Leung,K.Y., Barve,S.S. and Straley,S.C.
TITLE Molecular analysis of lcrGVH, the V antigen operon of Yersinia
JOURNAL J. Bacteriol. 171, 5646-5653 (1989)
MEDLINE 90008806
COMMENT Computer readable copy of sequence [J. Bacteriol. (1989) In press]
kindly submitted by Price,S.

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FEATURES
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-10_signal
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246 DPRKDEVFANRVITDDIELLKILAYFLPEDTILKGHYDNOLONGIKR 295
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396 YTDEIFRASAEEYKILKMPOTTIYVDSSEKTIYSIDPLGSEKKRFGAL 445
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seq_documentation_block:
LOCUS      A46411      1014 bp      DNA
DEFINITION Sequence 1 from Patent WO9524475.
ACCESSION      A46411
NID      92300612
VERSION      A46411.1 GI:2300612
KEYWORDS
SOURCE
ORGANISM      Yersinia pestis.
              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
              Yersinia pestis.
REFERENCE      1 (bases 1 to 1014)
AUTHORS      Tildall,R.W., Williamson,E.D. and Leary,S.E.
TITLE      VACCINE COMPOSITIONS
JOURNAL      Patent: WO 9524475-A 1 14-SEP-1995;
              SECR DEFENCE BRIT (GB)
COMMENT      Other publication AU 1853995 950925.
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55 PKRDEVFANRVITDDIELKKILAYFLPEDAILKGHYDNLONGIKRV 104
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105 KEFLSSPNTOWELRAFMAVMHFSLTADRIDDDILKYIVDSNMHHGDARS 154
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447 NLKNSYSYKNDNNELSHFATCSDKSRLPLNDLVSKTTQLSDITSRFNSA 496
255 NLKNSYSYKNDNNELSHFATCSDKSRLPLNDLVSKTTQLSDITSRFNSA 304
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seq_documentation_block:

LOCUS A46413 1014 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 3 from Patent WO9524475.
ACCESSION A46413
NID 92300614
VERSION A46413.1 GI:2300614

KEYWORDS

SOURCE

ORGANISM

Yersinia pestis.
Yersinia pestis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
1 (bases 1 to 1014)
Titball,R.W., Williamson,E.D. and Leary,S.E.
VACCINE COMPOSITIONS
Patent: WO 9524475-A 3 14-SEP-1995;
SECR DEFENCE BRIT (GB)
Other publication AU 1853995 950925.
Location/Qualifiers
1. 1014
/organism="Yersinia pestis"
/db_xref="taxon:632"
1. 987
/note="unnamed protein product; protein sequence is in
conflict with the conceptual translation"
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COMMENT
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CDS

BASE COUNT 343 a 184 c 205 g 282 t

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Quality: 1443.00 Length: 325
Ratio: 4.440 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.692

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DEFINITION Sequence 1 from Patent WO9628551.
ACCESSION A56793
NID 93712808
VERSION A56793.1 GI:3712808

KEYWORDS

SOURCE

ORGANISM

Yersinia pestis.
Yersinia pestis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
1 (bases 1 to 1014)
Titball,R.W., Williamson,E.D., Leary, Sophie,E.C., Oyston,P.C.,
Bennett and Alice,M.
VACCINES FOR PLAGUE
Patent: WO 9628551-A 1 19-SEP-1996;
SECR DEFENCE (GB)
Other publication ZA 9602036 960716
Other publication AU 4951196 961002.
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COMMENT

FEATURES

CDS

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Percent Similarity: 100.000 Percent Identity: 99.692

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ACCESSION A56795
NID 93712810
VERSION A56795.1 GI:3712810

KEYWORDS
SOURCE
ORGANISM

Yersinia pestis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.

REFERENCE 1 (bases 1 to 1014)

AUTHORS Titball, R.W., Williamson, E.D., Leary, Sophie, E.C., Oyston, P.C.,

TITLE VACCINES FOR PLAGUE

JOURNAL Patent: WO 9628551-A 3 19-SEP-1996;

SECR DEFENCE (GB)

COMMENT Other publication ZA 9602036 960716

Other publication AU 4951196 961002.

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BASE COUNT 343 a 184 c 205 g 282 t

ORIGIN

alignment_scores:
Quality: 1443.00 Length: 325
Ratio: 4.440 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.692

alignment_block:
US-08-699-716A-2 x A56795 (1) ..

Align seg 1/1 to: A56795 from: 1 to: 1014

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|||||
55  PRKSEVFNANRVITDDIELKKILAYFLPEDAILKGHYDNOLONGIKRV 104
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155  KLREELAEITAEIKIYVIOAEINKHLSSSGTINIHDKSINLMKKNLYGY 204
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447  NLKNSYSYKDNNELSHFATCSDKSRPLNDLVSOQTQLSDITSRFNSA 496
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seq_documentation_block:

LOCUS YPCD1 70305 bp DNA BCT 03-SEP-1999
DEFINITION Yersinia pestis plasmid pCD1.
ACCESSION A117189
NID 95832423

VERSION A117189.1 GI:5832423

KEYWORDS

Chapterone; cytotoxic effector; ISI00; ISI616; ISI617; lcr;

low-calcium response; syc; targeted effector; transposase; type III

secretion; V antigen; virulence; ylp; yop; ysc.

Yersinia pestis.

Yersinia pestis

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

Yersinia.

REFERENCE 1 (bases 1 to 70305)

AUTHORS Karlyshev, A.V. and Wren, B.W.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 70305)

AUTHORS Baker, S.G. and Mungall, K.

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 70305)

AUTHORS James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.

TITLE Direct Submission

JOURNAL

Submitted (03-SEP-1999) *Yersinia pestis* sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA
E-mail: barrell@sanger.ac.uk DNA supplied by Dr. Andrey Karlyshev and Prof. Brendan Wren, [3]. Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, Keppel Street, London WC1E 7HT
Notes:

COMMENT

Yersinia pestis sequencing at The Sanger Centre is funded by Biowulf Genomics
Details of *Y. pestis* sequencing at the Sanger Centre are available on the World Wide Web.
(URL: <http://www.sanger.ac.uk/Projects/Y-pestis/>)
CDS are numbered using the following system eg yPCP1.01c, yP (*Y. pestis*), pCP1 (plasmid name), .01 (first CDS), c (complementary strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or att) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

FEATURES

source

Location/Qualifiers

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/note="IS100 element"

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88..1110

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2693.4 E(): 0, 100.0% identity in 259 aa overlap. Similar to many others e.g. IS7B_ECOLI (EMBL:X14793), IS21, E.coli

transposase for insertion sequence element IS21 (265 aa) (47.4% identity in 249 aa overlap). Contains P500017

ATP/GTP-binding site motif A (P-loop)"

ATP/GTP-binding site motif A (P-loop)"

ATP/GTP-binding site motif A (P-loop)"

ATP/GTP-binding site motif A (P-loop)"

ATP/GTP-binding site motif A (P-loop)"

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Ratio: 4.448          Gaps: 0
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            Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Brubaker,R.R. and Garcia,E.
            Structural organization of virulence-associated plasmids of
            Yersinia pestis
            J Bacteriol. 180 (19), 5192-5202 (1998)
JOURNAL    MEDLINE
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            Hu,P., Elliott,J., McCready,P., Skowronski,E., Garnes,J.,
            Kobayashi,A., Carrano,A.V., Brubaker,R. and Garcia,E.
            Direct Submission
            Submitted (16-MAR-1998) Biology and Biotechnology, Lawrence
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ELISAQODAKIILADAEVYEQOKGOWMGMEARLTQTLIHTOLOQOQYRHY
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|||||

8487 DPKRDSVFANRVITDDIELLKILAFLEPEDAILKGGHIDNOLQNGIKR 8536
296 VKEFLESSPTQWELARAFMAVMHESLTADRIDDDILKVIYDSNMHGDAR 345
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346 SKUREELAEITAEIKIYSVIOAEINKHLSSGTTINHDKSNLMDKNLYG 395
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396 YTPDEIRKASAEYKILEKMPOTTIOVDGSEKKIYSINDPFGSEKKRFGAL 445
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8637 YTPDEIRKASAEYKILEKMPOTTIOVDGSEKKIYSINDPFGSEKKRFGAL 8686
446 GNLKNSYSYKNNNELSHFATCSDKSRPLNDLYSQKTTQLSDITSRPNFS 495
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8687 GNLKNSYSYKNNNELSHFATCSDKSRPLNDLYSQKTTQLSDITSRPNFS 8736
496 AIEALNRFIOKYDSVMORLIDDTSGK 521
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8737 AIEALNRFIOKYDSVMORLIDDTSGK 8762
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seq_documentation_block:
LOCUS AF074612 70559 bp DNA circular BCT 03-NOV-1998
DEFINITION Yersinia pestis plasmid pCD1, complete plasmid sequence.
ACCESSION AF074612
NID 93822037
VERSION AF074612.1 GI:3822037
KEYWORDS
SOURCE Yersinia pestis.
ORGANISM Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE
AUTHORS 1 (bases 1 to 70559)
Perry,R.D., Straley,S.C., Fetherston,J.D., Rose,D.J., Gregor,J. and
Blattner,F.R.
TITLE DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1
of Yersinia pestis KIM5
JOURNAL Infect. Immun. 66 (10), 4611-4623 (1998)
MEDLINE 98427122
REFERENCE 2 (bases 1 to 70559)
Perry,R.D., Straley,S.C., Fetherston,J.D., Rose,D.J., Gregor,J. and
Blattner,F.R.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1998) Microbiology and Immunology, University of
Kentucky, MS415 Medical Center, Lexington, KY 40536-0084, USA
COMMENT Unique identifiers, starting at Y0001, are assigned to each gene of
pCD1.
FEATURES
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Location/Qualifiers
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/plasmid="pCD1"
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an approx. 200 aa protein GENPEPT: g1|537126,orf_0198
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LDVSPVAVAARSRKVEWENOQREKORLPLEMDLILAKARFVREPRRSYOTERKAH
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CDS 4758 . 5186
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Quality: 1450.00 Length: 326
Ratio: 4.448 Gaps: 0
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246 DPRKDSEVFANRVITDDIELKKILAYFLPEDTILKGGHYNOQLNGIKR 295
|||||
12690 DPRKDSEVFANRVITDDIELKKILAYFLPEDTILKGGHYNOQLNGIKR 12739
296 VKPELSSPNTQWELRAFMVAFHPSLTADRIDDILKVIYDSNMHGDAR 345
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346 SKLREELAEFLAEIKIYSVIOAEINKHLSSTGTTINIDKSNIMDKNLYG 395
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396 YTDEIFKASAEYKILEKPPOTTIOVDGSEKKIYSIKDFLGSENKRTGAL 445
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12840 YTDEIFKASAEYKILEKPPOTTIOVDGSEKKIYSINDFLGSEKKRTGAL 12889
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12890 GNLKNSIYNNDDNLSHFATTCSDKSRPLNDIVSQKTTQSDITSRFS 12939
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LOCUS YPRPIVANT 981 bp DNA BCT 13-MAR-1997
DEFINITION Y.pseudotuberculosis v antigen gene.
ACCESSION X96802
NID G1405834
VERSION X96802.1 GI:1405834
KEYWORDS
SOURCE Yersinia pseudotuberculosis.
ORGANISM Yersinia pseudotuberculosis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE
1 (bases 1 to 981)
Roggenkamp, A., Geiger, A.M., Leitritz, L., Kessler, A. and
Heesemann, U.
Passive immunity to infection with Yersinia spp. mediated by
anti-recombinant v antigen is dependent on polymorphism of v
antigen
JOURNAL Infect. Immun. 65 (2), 446-451 (1997)
MEDLINE 97162308
REFERENCE 2 (bases 1 to 981)
Roggenkamp, A.
AUTHORS Direct Submission
TITLE Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology,
JOURNAL University of Muenzberg, Josef-Schneider Strasse 2, 97080
Muenzberg, FRG
FEATURES
Location/Qualifiers

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alignment_scores: Quality: 1418.00 Length: 326 Ratio: 4.390 Gaps: 0 Percent Similarity: 99.080 Percent Identity: 96.626

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246 DPKRDEVFANRVITDDIELKILAFLEPDTILKGHYDNOQNGIKR 295
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296 VKEFLESPNTQWELRAFAVYHFSLTADRIDDLIKVIVDSMNHGDAR 345
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346 SKLRELAELTALKIYSVIOAEINKHLSGGTINIHDKSINIMDKNLGY 395
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396 YDEIFKSAEYKILIEKMPOTTIOVDSSEKKIYSIKDFIGSENKRTGAL 445
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201 YDEIFKSAEYKILIEKMPOTTIOVDSSEKKIYSIKDFIGSENKRTGAL 250
446 GNLKNSYSYNKDNNELSHFATTCSDKSRPLNDVSOKTTQSLDITSRFS 495
|||||
251 GNLKNSYSYNKDNNELSHFATTCSDKSRPLNDVSOKTTQSLDITSRFS 300
496 ALEALNRFIOKYDSVMORLLDPTSGK 521
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301 ALEALNRFIOKYDSVMORLLDPTSGK 326

seq_name: gb_ba1:YEPICRGVHP

seq_documentation_block: LOCUS YEPICRGVHP 2201 bp DNA BCT 26-APR-1993 DEFINITION Yersinia pseudotuberculosis V-antigen (LcrG, LcrV, LcrH) genes, complete cds. ACCESSION M57893 NID G155456 VERSION M57893.1 GI:155456 KEYWORDS V-antigen. Yersinia pseudotuberculosis (strain YPIII (pIB1) DNA. SOURCE Yersinia pseudotuberculosis ORGANISM Yersinia pseudotuberculosis

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Yersinia. REFERENCE 1 (bases 1 to 2201) AUTHORS Bergman,T., Hakansson,S., Forsberg,A., Norlander,L., Macellaro,A., Baeckman,A., Boelin,I and Wolf-Watz,H. TITLE Analysis of the V antigen lcrGVH-yopBD Operon of Yersinia pseudotuberculosis: Evidence for a regulatory role of LcrH and LcrV JOURNAL J. Bacteriol. 173, 1607-1616 (1991) MEDLINE 91154114 FEATURES source location/Qualifiers 1. .2201 /organism="Yersinia pseudotuberculosis" /strain="YPIII (pIB1)" /db_xref="taxon:633" 219. .224 /gene="lcr operon" 219. .258 /gene="lcr operon" 241. .246 /gene="lcr operon" 252. .258 /gene="lcr operon" 264. .551 /gene="lcrG" 264. .551 /gene="lcrG" /codon_start=1 /transl_table=1 /evidence=experimental /product="V-antigen" /protein_id="AA27644.1" /db_xref="PID:g155457" /db_xref="GI:155457" /translation="MKSSHFDYDKTLKQAEALIASDSIRAKILOEMCADIGTPEAV MKTFGRSADEIIPARELDEIKRQERQPOHPYDGKRPKPTMNGQII" 553. .1533 /gene="lcrV" 553. .1533 /gene="lcrV" /codon_start=1 /transl_table=1 /evidence=experimental /product="V-antigen" /protein_id="AA27645.1" /db_xref="PID:g155458" /db_xref="GI:155458" /translation="MIRAYEQNPQHFIEDLEKRVVOLTGHGSSVLEELVOLVKDKNI DISIKYDPRKDEVFANRVITDDIELKILAFLEPDAILKGHYDNOQNGIKRKY EFLESPNTQWELRAFAVYHFSLTADRIDDLIKVIVDSMNHGDARSKLRELAEL TALKIYSVIOAEINKHLSGGTINIHDKSINIMDKNLGYTDEIFKSAEYKILIEK MPOTTQEGTEKTIYSIKNFLESEKRTGALGNLKDYSYNKDNNELSHFATTCSDK SRPLNDVSOKTTQSLDITSRFSALNALNRFIOKYDSVMORLLDPTSGK" 1546. .2052 /gene="lcrH" 1546. .2052 /gene="lcrH" /codon_start=1 /transl_table=1 /evidence=experimental /product="V-antigen" /protein_id="AA27646.1" /db_xref="PID:g155459" /db_xref="GI:155459" /translation="MOEETTDQEOVLAMESFLKGGGTAMLEISSDTLEQYSLAF NOYOSGRYDEAHKVFQALCVLDHYDSRFFLGACACQAMGOYDLAIHSYSYCAIMDIK EEPFEPHAECULLQKGLAEASGFLAQLIADKPEFRELSTRVSSMELATLKLEM EHECVNP"

BASE COUNT 714 a 450 c 485 g 552 t

ORIGIN

alignment_scores: Quality: 1418.00 Length: 326

Ratio:	4.390	Gaps:	0
Parity:	99.080	Percent Identity:	96.626

alignment_block:
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Align seg 1/1 to: YEPLCRGVHP from: 1 to: 2201

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285 VKEFLESSENTOMELRAFMAVHFSLTADRIDDDILKIVYDSNNHHGDAR 334
346 SKURELALIELTAEIKYVIOAEINKHSSSGTINIHDKSINIMDKNLIG 395
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396 YTDEEFKSAEKKILEKMPOTTIOVGSKKIVSIKDFGSEKKRTGAL 445
385 YTDEEFKSAEKKILEKMPOTTIOGTEKTKIVSIKNFLESKKRTGAL 434
446 GNLKNSYVKNKDNNELSHFATCSDKSRPLNDLVSOIKTOLSDITSRFS 495
435 GNLKNSYVKNKDNNELSHFATCSDKSRPLNDLVSOIKTOLSDITSRFS 484
496 AIEALNRFIOKYDSVMORLLDITSGK 521
485 AIEALNRFIOKYDSVMORLLDITSGK 510

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seq_name: gb_baz:AF102990

seq_documentation_block:

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DEFINITION	Yersinia enterocolitica plasmid pYae227, complete sequence.					
ACCESSION	AF102390	AF054978	AF054979	AF054980	AF054981	AF080155
						269926
						106216

NID 94324323

KEYWORDS
SOURCE
Versinia enterocolitica.

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 32056 to 32871)	Cornelis, G., Sluiter, C., de Rouvroit, C. L. and Michiels, T.	Homology between vif, the transcriptional activator of the	
		Yersinia virulence regulon, and ArcC, the Escherichia coli	
		arabinose operon regulator	
	J. Bacteriol. 171 (1), 254-262 (1989)		

REFERENCE	2 (bases 15074 to 15994)
AUTHORS	Hakansson, S., Bergman, T., Vanooteghem, J.C., Cornelis, G. and

TITLE YopB and YopD constitute a novel class of Yersinia Yop proteins
JOURNAL Infect. Immun. 61 (1), 71-80 (1993)

TITLE
SYCE, a chaperone-like protein of *Yersinia enterocolitica* involved
in the secretion of YOPs
JOURNAL
Mol. Microbiol. 8 (1), 123-131 (1993)

REFERENCE 4 (bases 23950 to 25269)

TITLE • YSCN, the putative energizer of the Yersinia Yop secretion

machinery
J. Bacteriol. 176 (6), 1561-1569 (1994)

REFERENCE	5 (bases 29897 to 30961)
AUTHORS	Aliaoui, A., Moestyn, S., Sluitters, C. and Cornelis, G.R.
TITLE	Vscu, a Yersinia enterocolitica inner membrane protein involved in top secretion
JOURNAL	J. Bacteriol. 176 (15), 4534-4542 (1994)

REFERENCE	6 (bases 43292 to 43717)
AUTHORS	Mattila,P., Benier,B., Deslee,P., Michiels,T. and Cornelis,G.R
TITLE	Individual chaperones required for Yop secretion by <i>Yersinia</i>
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 91 (22), 10493-10497 (1994)
MEDLINE	95024141
REFERENCE	7 (bases 31537 to 31932)

REFERENCE	7 (Pages 31537 to 31933)
AUTHORS	Allaoui A., Scheen R., Lambert de Rouvroit C. and Cornelis G.R.
TITLE	Virg, a Yersinia enterocolitica lipoprotein involved in Ca ²⁺ -dependency, is related to exsB of Pseudomonas aeruginosa
JOURNAL	J. Bacteriol. 177 (15), 4230-4237 (1995)

REFERENCE	AUTHORS	TITLE	JOURNAL
8 (bases 53135 to 53437)	Stahner, I., Iriarte, M. and Cornelis, G. R.	YscM and YscN2, two Yersinia enterocolitica proteins causing downregulation of yop transcription	Mol. Microbiol. 26 (4), 833-843 (1997)

REFERENCE 9 (bases 18681 to 18968)

AUTHORS	Boyd, A.P., Sory, M.P., Iriarte, M. and Cornelis, G.R.
TITLE	Heparin interferes with translocation of Yop proteins into Hela cells and binds to LcrG, a regulatory component of the Yersinia Yop apparatus

MEDLINE 98143428
REFERENCE 10 (pages 22612 to 22890)
AUTHORS Iliarte, M., Sotry, M.P., Boland, A., Boyd, A.P., Mills, S.D.,
Lambermont, I., and Cornelius, G.R.
TITLE I κ B α , a protein involved in control of Yop release and in
translocation of Yersinia Yop effectors
JOURNAL EMBO J. 17 (7), 1907-1918 (1998)

REFERENCE	11 (pages 1 to 69673)
AUTHORS	Irlate, M., Lambermont, I., Kerdbourch, C. and Cornelis, G.R.
TITLE	detailed genetic map of the pIyee27 plasmid of <i>Yersinia enterocolitica</i> serotype O:9
JOURNAL	Unpublished

REFERENCE	AUTHORS	TITLE	JOURNAL
12 (pages 1 to 69673)	Iriarte, M., Lambert, I., Kerporch, C. and Cornells, G. R.	Direct Submission	Submitted (30-OCT-1999) Microbial Pathogenesis Unit, Christian de Duve Institute of Cellular Pathology and Faculté de Médecine, Université Catholique de Louvain, Av. Hippocrate 74.49, Brussels 1200, Belgium

COMMENT

on May 18, 1999 this sequence version replaced q1:3411136
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q1:3603357 q1:2738986 q1:2944089 q1:3411138 q1:3108216 q1:4372001
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FEATURES	Location/Qualifiers
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CDS

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CDS

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||:|||||
6176 DPRKSEYFANRYTDDIELKILAYFLPEDTILKGGHYDQNLQNGIKR 6127
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236 VKPELSSPNTQWELRAFMVNHESLTADRIDDDLKVIYVDSMNHGDAK 345
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396 YTDEELFKASAEYKILKMPOTTIOVDSSEKKIYVSIKDPISGNRTGAL 445
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DEFINITION Y.enteroocollitica v antigen gene, strain Y-96-P.
ACCESSION X96801
NID g1405830
VERSION X96801.1 GI:1405830
KEYWORDS v antigen.
SOURCE Yersinia enterocolitica.
ORGANISM Yersinia enterocolitica
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE 1 (bases 1 to 975)

AUTHORS Rogenkamp,A., Geiger,A.M., Leitritz,L., Kessler,A. and Heesemann,J.
TITLE Passive immunity to infection with Yersinia spp. mediated by anti-recombinant V antigen is dependent on polymorphism of V antigen
JOURNAL Infect. Immun. 65 (2), 446-451 (1997)
MEDLINE 97162308
REFERENCE 2 (bases 1 to 975)
AUTHORS Rogenkamp,A.
JOURNAL Direct Submission
Submitted (22-MAR-1996) A. Rogenkamp, Hygiene and Microbiology, University of Wuerzburg, Josef-Schneider Strasse 2, 97080 Wuerzburg, FRG
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446 GNLKNSYVKNNNELSHGCTCSDKSRPLNDVSKTQLSDITSRFS 495
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301 AIEALNRFIOKYDSVQWRLLDPT 323
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ACCESSION X96798
MID G1405828
VERSION X96798.1 GI:1405828
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SOURCE Yersinia enterocolitica.
ORGANISM Yersinia enterocolitica.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE 1 (bases 1 to 975)
AUTHORS Rogenkamp,A., Geiger,A.M., Leitritz,L., Kessler,A. and Heesemann,J.
TITLE Passive immunity to infection with Yersinia spp. mediated by anti-recombinant V antigen is dependent on polymorphism of V antigen
JOURNAL Infect. Immun. 65 (2), 446-451 (1997)
MEDLINE 97162308
REFERENCE 2 (bases 1 to 975)
AUTHORS Rogenkamp,A.
JOURNAL Direct Submission
Submitted (22-MAR-1996) A. Rogenkamp, Hygiene and Microbiology, University of Wuerzburg, Josef-Schneider Strasse 2, 97080 Wuerzburg, FRG
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US-08-699-716a-2 x YE808VANT (1) ..
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JOURNAL Unpublished (1997)
COMMENT On Mar 10, 1998 this sequence version replaced gi:2948191.

CONTACT: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
hit genomic sequence AC006066
Plate: 23 row: B column: 8
High quality sequence stop: 490.

FEATURES
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ACCESSION AA391919
NID g2044894
VERSION AA391919.1 GI:2044894
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 442)
Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,
Brokstein, P., Lewis, S. and Rubin, G.M.
BDGP/HMI Drosophila EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1400810.

JOURNAL
COMMENT

CONTACT: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu

Plate: 108 row: C column: 4
High quality sequence stop: 264.

FEATURES
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/lab_host="SOLR"
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BASE COUNT 97 a 136 c 130 g 79 t

ORIGIN

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seq_documentation_block:
LOCUS A0037853 587 bp mRNA EST 29-MAR-1999
DEFINITION A0037853 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSE372, mRNA sequence.
ACCESSION A0037853
NID g3984606
VERSION A0037853.1 GI:3984606
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
Eukaryota; Dictyostelida; Dictyostelium.
REFERENCE 1 (bases 1 to 587)
Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M.,
Yoshino, R., Mita, B.N., Pi, M., Saito, T., Takemoto, K., Yasukawa, H.,
Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
The Dictyostelium developmental cDNA project: generation and
analysis of expressed sequence tags from the first-finger stage of
development
JOURNAL DNA Res. 5 (6), 335-340 (1998)
MEDLINE 99156227
COMMENT On Jan 5, 1998 this sequence version replaced gi:2747254.

JOURNAL
COMMENT

CONTACT: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-noda, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'.
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us-08-699-716a-2 x AU037853 (3) ..

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seq_name: gb_est19:AA538585

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 ACCESSION Drosophila melanogaster cDNA clone LD18150 5prime, mRNA sequence.
 AA538585
 NID 92794780
 VERSION AA538585.1 GI:2794780
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 605)
 Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
 Broksstein,P., Lewis,S. and Rubin,G.M.
 BDGP/HMI Drosophila EST Project
 Unpublished (1997)

TITLE
 JOURNAL
 COMMENT On Jan 19, 1998 this sequence version replaced gi:2285101.

Contact: Harvey, D.
 G. M. Rubin-Molecular and Cell Biology
 University of California Berkeley
 539 LSA, Berkeley, CA 94720-3200, USA
 Fax: 510 643 9947
 Email: http://www.fruitfly.org/EST_estfruitfly.berkeley.edu
 Plate: 181 row: E column: 2
 High quality sequence stop: 419.
 Location/Qualifiers

FEATURES

source

1. 605
 /organism="Drosophila melanogaster"
 /db_xref="BDGP_EST:BDc1n017283"
 /db_xref="taxon:7227"
 /clone="LD18150"
 /clone_lib="LD Drosophila melanogaster embryo Bluescript"
 /sex="male and female"
 /dev_stage="0 to 24 hours mixed stage embryonic"
 /lab_host="SOLR"
 /note="Organ: embryo; Vector: Bluescript SK; Site:1;
 EcoRI; Site:2: XhoI; Constructed using Stratagene ZAP-cDNA
 Synthesis kit. Oligo dt-primed and directionally cloned at
 EcoRI and XhoI in Bluescript SK(+/-)"
 BASE COUNT 145 a 183 c 166 g 110 t 1 others
 ORIGIN

alignment_scores:
 Quality: 77.00 Length: 28
 Ratio: 3.208 Gaps: 0
 Percent Similarity: 85.714 Percent Identity: 53.571

alignment_block:
 us-08-699-716a-2 x AA538585 (2) ..

Align seg 1/1 to: AA538585 from: 1 to: 605

2 GHHHHHHHSGHIDDDKMKRISS 29
 ||| |||||:::|:|:|:|
 102 GHXHHHHHHTSANYDGLDTHNLKLP 129

seq_name: gb_est11:AA201964

seq_documentation_block:

LOCUS AA201964 437 bp mRNA EST 29-NOV-1998
 DEFINITION LD05053.5prime LD Drosophila melanogaster embryo Bluescript
 ACCESSION Drosophila melanogaster cDNA clone LD05053 5prime, mRNA sequence.
 AA201964
 NID 91797767
 VERSION AA201964.1 GI:1797767
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 437)
 Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
 Broksstein,P., Lewis,S. and Rubin,G.M.
 BDGP/HMI Drosophila EST Project
 Unpublished (1997)

On May 18, 1995 this sequence version replaced gi:811639.

Contact: Harvey, D.
 G. M. Rubin-Molecular and Cell Biology
 University of California Berkeley
 539 LSA, Berkeley, CA 94720-3200, USA
 Fax: 510 643 9947
 Email: http://www.fruitfly.org/EST_estfruitfly.berkeley.edu
 Plate: 50 row: E column: 5
 High quality sequence stop: 417.
 Location/Qualifiers

FEATURES

source

1. 437
 /organism="Drosophila melanogaster"
 /db_xref="BDGP_EST:BDc1n004432"
 /db_xref="taxon:7227"
 /clone="LD05053"
 /clone_lib="LD Drosophila melanogaster embryo Bluescript"
 /sex="male and female"
 /dev_stage="0 to 24 hours mixed stage embryonic"
 /lab_host="SOLR"
 /note="Organ: embryo; Vector: Bluescript SK; Site:1;
 EcoRI; Site:2: XhoI; Constructed using Stratagene ZAP-cDNA
 Synthesis kit. Oligo dt-primed and directionally cloned at
 EcoRI and XhoI in Bluescript SK(+/-)"
 BASE COUNT 98 a 132 c 128 g 79 t
 ORIGIN

alignment_scores:
 Quality: 75.00 Length: 28
 Ratio: 3.125 Gaps: 0
 Percent Similarity: 85.714 Percent Identity: 53.571

alignment_block:

us-08-699-716a-2 x AA201964 (1) ..

Align seg 1/1 to: AA201964 from: 1 to: 437

2 GHHHHHHHSGHIDDDKMKRISS 29
 ||| |||||:::|:|:|:|
 109 GHGHHHHHHTSANYDGLDTHNLKLP 136

seq_name: gb_est24:AI182515

seq_documentation_block:

LOCUS AI182515 440 bp mRNA EST 08-OCT-1998
 DEFINITION ue21g12.x1 sugano mouse kidney mklia Mus musculus cDNA clone

IMAGE:1481062 3', mRNA sequence.

ACCESSION A1182515
NID 93733153
VERSION A1182515.1 GI:3733153
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 440)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMHI Mouse EST Project
Unpublished (1996)
On Jan 14, 1998 this sequence version replaced gi:2754392.

TITLE JOURNAL
COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMHI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:929418
Seq primer: custom primer used
High quality sequence stop: 420.

FEATURES
source
Location/Qualifiers
1..440
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1481062"
/clone_1lb="Sugano mouse kidney mk1a"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pME185-FL3; Site 1: DraIII
(CACATGCG); Site 2: DraIII (CACATGCG); 1st strand cDNA
was primed with an oligo(dt) primer
[ATGTGGCTTTTCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor (TGTGGCTACTG6), digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACATGCG, 3' site CACATGCG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTGTGCTCTTAAAGCTGCG and 3' end
primer CGACCTGACGCTGACGACG."

BASE COUNT 91 a 94 c 104 g 151 t
ORIGIN

alignment_scores:
Quality: 75.00 Length: 24
Ratio: 3.947 Gaps: 0
Percent Similarity: 79.167 Percent Identity: 50.000

alignment_block:
us-08-699-716a-2 x A1182515/rev (6) ..
Align seg 1/1 to reverse of: A1182515 from: 1 to: 440

3 HHHHHHHHSSGHIDDDDKMKMK 26
||||| : : : : :
136 HHHHHHHHSSGHIDDDDKMK 113
seq_name: gb_est14:AA441519

seq_documentation_block:
LOCUS AA441519 491 bp mRNA EST 28-NOV-1998
DEFINITION LD16485.5prime LD Drosophila melanogaster embryo Bluescript
Drosophila melanogaster cDNA clone LD16485 5prime, mRNA sequence.
ACCESSION AA441519
NID 92153397
VERSION AA441519.1 GI:2153397
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 491)
Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
Brokslein,P., Lewis,S. and Rubin,G.M.
BDGP/HMHI Drosophila EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1395398.

TITLE JOURNAL
COMMENT

Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 USA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 164 row: H column: 1
High quality sequence stop: 363.

FEATURES
source
Location/Qualifiers
1..491
/organism="Drosophila melanogaster"
/db_xref="BDGP_EST:BDc1n015696"
/db_xref="taxon:7227"
/clone="LD16485"
/clone_1lb="LD Drosophila melanogaster embryo Bluescript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
/note="Organ: embryo; Vector: Bluescript SK; Site 1:
EcoRI; Site 2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis kit. Oligo dt-primed and directionally cloned at
EcoRI and XhoI in Bluescript SK(+/-)"

BASE COUNT 104 a 153 c 138 g 94 t
ORIGIN

alignment_scores:
Quality: 75.00 Length: 28
Ratio: 3.125 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 53.571

alignment_block:
us-08-699-716a-2 x AA441519 (2) ..
Align seg 1/1 to: AA441519 from: 1 to: 491

2 GHHHHHHHSSGHIDDDDKMKRISS 29
||||| : : : : :
100 GHHHHHHHSSGHIDDDDKMKRISS 127
seq_name: gb_est14:AA439056

seq_documentation_block:
LOCUS AA439056 499 bp mRNA EST 28-NOV-1998
DEFINITION LD13501.5prime LD Drosophila melanogaster embryo Bluescript
Drosophila melanogaster cDNA clone LD13501 5prime, mRNA sequence.
ACCESSION AA439056
NID 92150937
VERSION AA439056.1 GI:2150937
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,
Brockstein, P., Lewis, S. and Rubin, G.M.
BDGP/HMMI Drosophila Est Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1393447.

Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
Plate: 135 row: A column: 1
High quality sequence stop: 427.

FEATURES	Location/Qualifiers
source	1. .499

BASE COUNT	107 a	154 c	145 g	93 t
/note="Organ: embryo; Vector: Bluescript SR; Site_1: EcoRI; Site_2: XhoI; Constructed using Stratagene ZAP-CDNA Synthesis kit; oligo dt-primed and directionally cloned at EcoRI and XhoI in Bluescript SR(+/-)"				

Align seg 1/1 to: AA439056 from: 1 to: 499

```

2  GHHHHHHHHHSSGHHDDDDKHHMKISS 29
   || |||||:|:::|:|:|:|:|:|:|:|
100 GHHGHHHHHHHTSANDVGLDTHNLKLP 127

```

seq_name: gb_est18:AA735384

```
seq_documentation_block:
```

LOCUS	AA735384	506 bp	mRNA	EST	27-NOV-1998
DEFINITION	LD21220.5prime LD Drosophila melanogaster embryo pot2 Drosophila melanogaster cDNA clone LD21220 5prime, mRNA sequence.				

VERSION	AA735384.1	GI:2761314
---------	------------	------------

KEYWORDS	EST.
SOURCE	fruit fly.
ORGANISM	<i>Drosophila melanogaster</i>

REFERENCE 1 (pages 1 to 506)
AUTHORS Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,
Brokslein, P., Lewis, S. and Rubin, G. M.
TITLE BDGP/HMM Drosophila EST Project
JOURNAL Unpublished (1997)
COMMENT On Jan 5, 1998 this sequence version replaced gl:2581344
Contact: Harvey, D.

G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: 212 row: B column: 393.
High quality sequence stop: 393.

```

FEATURES
source      location/Qualifiers
1. .506

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PAGE	COLUMN	LINE	DATE	TIME	BY	REMARKS
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104	1	104	104	104	104	104
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123	1	123	123	123	123	123
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126	1	126	126	126	126	126
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134	1	134	134	134	134	134
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147	1	147	147	147	147	147
148	1	148	148	148	148	148
149	1	149	149	149	149	149
150	1	150	150	150	150	150
151	1	151	151	151	151	151
152	1	152	152	152	152	152
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154	1	154	154	154	154	154
155	1	155	155	155	155	155
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157	1	157	157	157	157	157
158	1	158	158	158	158	158
159						

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alignment_scores:
    quality: 75.00
    ratio: 3.125
Percent Similarity: 85.714
    Percent Identity: 53.571
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Align seg 1/1 to: AA735384 from: 1 to: 506

```

2  GHHHHHHHHHSSGHHDDDDKHKMKISS  29
   || | || || | : : : : | : : :
86 GHHGHHHHHHHTSANDGLDTHNLKLP  113

```

seq_name: gb_est21:AA948995

seq_documentation_block

LOCUS	AA948995	523 bp	MRNA	EST	25-NOV-1998
DEFINITION	LD27722.5prime LD Drosophila melanogaster embryo POT2 Drosophila melanogaster cDNA LD27722 5prime, mRNA sequence.				

VERSION AA948995.1 GI:3110904

KEYWORDS	EST.
SOURCE	fruit fly.
ORGANISM	<i>Drosophila melanogaster</i>

REFERENCE 1 (bases 1 to 523)
 AUTHORS Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
 Brokstein,P., Lewis,S. and Rudin,G.M.
 TITLE BDGP/HMT Drosophila EST Project
 JOURNAL Unpublished (1997)
 COMMENT On Jan 19, 1998 this sequence version replaced gi:2284655

G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
Plate: 277 row: B column: 10
High quality sequence stop: 512.

location/Qualifiers

1. 523

source

/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="ID27722"
/clone_lib="UD Drosophila melanogaster embryo pot2"

```

FEATURES
  source      location/Qualifiers
              1..523
              /organism="Drosophila melanogaster"
              /db_xref="taxon:7227"
              /clone="ID27722"
              /clone_lib="LD Drosophila melanogaster embryo pot2

```

```

BASE COUNT      114 a      165 c      148 g      96 t
ORIGIN

alignment_scores:
    Quality:      75.00      Length:      28
    Ratio:        3.125      Gaps:      0
    Percent Similarity: 85.714      Percent Identity: 53.571

alignment_block:
US-08-699-716A-2 x AA948995 (3) ..

Align seg 1/1 to: AA948995 from: 1 to: 523

      2 GHHNNHHNHHSSGHIDDDKHMKRTSS 29
          ||| |||||:::|::| |:::
      100 GHNGHHNHHHTSANVDGLDTNLKLPRA 127

seq_name: gb_est20:AA820589

seq_documentation_block:
LOCUS      AA820589      554 bp      mRNA      EST      25-NOV-1998
DEFINITION LD24394.sprime LD Drosophila melanogaster embryo POT2 Drosophila
            melanogaster CDNA clone LD24394 Sprime, mRNA sequence.
ACCESSION   AA820589
VERSION     g2890457
KEYWORDS    AA820589.1 GI:2890457
SOURCE      EST.
ORGANISM    fruit fly.
            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Ephydriidae; Drosophila.
1 (bases 1 to 554)
Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
Broksstein,P., Lewis,S. and Rubin,G.M.
BCGP/HMT Drosophila EST Project
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2152541.

TITLE      JOURNAL
COMMENT    Contact: Harvey, D.
           G. M. Rubin-Molecular and Cell Biology
           University of California Berkeley
           539 LSA, Berkeley, CA 94720-3200, USA
           Fax: 510 643 9947
           Email: http://www.fruitfly.org/EST, estefruitfly.berkeley.edu
           Plate: 243 row: H column: 10
           High quality sequence stop: 448.
           Location/Qualifiers
               1..554
                   /organism="Drosophila melanogaster"
                   /db_xref="taxon:7227"
                   /map="11 q13.4-q23.2"
                   /clone="LD24394"
                   /clone_lib="LD Drosophila melanogaster embryo POT2"
                   /sex="male and female"
                   /dev_stage="0 to 24 hours mixed stage embryonic"
                   /lab_host="Xl1 Blue"
                   /note="Organ: embryo; Vector: POT2; Site_1: EcoRI; Site_2
XhoI; Sized fractionated cDNAs were directly ligated into
POT2."
BASE COUNT      129 a      171 c      156 g      98 t
ORIGIN

Alignment_scores:
Quality:      75.00      Length:      28
Ratio:        3.125      Gaps:      0
Percent Similarity: 85.714      Percent Identity: 53.571

```

```

Ratio: 3.125      Gaps: 0
Percent Similarity: 85.714      Percent Identity: 53.571

Alignment_block:
US-08-699-716A-2 x AA820589 (3) ..

Align seg 1/1 to: AA820589 from: 1 to: 554

2 GHHNNHHHHSSGHIDDDDKHMKKISS 29
|||||:||||:||||:||||:||||:
101 GHGHHHHHHHTSANDGIDTHTNLKPLA 128

seq_name: gb_est1:AA264342

seq_documentation_block:
LOCUS AA264342 563 bp mRNA EST 29-NOV-1998
DEFINITION LD Drosophila melanogaster embryo Bluescript
Drosophila melanogaster cDNA clone LD07582 5prime, mRNA sequence.
ACCESSION G1900420
VERSION AA264342.1 GI:1900420
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 563)
Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
Brokstein,P., Lewis,S. and Rubin,G.M.
BDGP/HMT Drosophila EST Project
Unpublished (1997)
On May 8, 1995 this sequence version replaced gi:801550.

TITLE
JOURNAL
COMMENT

FEATURES
Source
1..563
/organism="Drosophila melanogaster"
/db_xref="BDGP_EST:BDcIn006957"
/db_xref="taxon:7227"
/cclone="LD07582"
/clone_id="LD Drosophila melanogaster embryo Bluescript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
/note="Organ: embryo. Vector: Bluescript SK. Site_1:
ECORI, Site_2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis kit. oligo dt-primed and directionally cloned at
ECORI and XhoI in Bluescript SK(+/-)"
BASE COUNT 130 a 175 c 155 g 103 t
ORIGIN

Alignment_scores:
Quality: 75.00 Length: 28
Ratio: 3.125 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 53.571

Alignment_block:
US-08-699-716A-2 x AA264342 (1) ..

Align seg 1/1 to: AA264342 from: 1 to: 563

2 GHHNNHHHHSSGHIDDDDKHMKKISS 29
|||||:||||:||||:||||:||||:
112 GHGHHHHHHHTSANDGIDTHTNLKPLA 139

```

```

seq_name: gb_est19:AA264985
seq_documentation_block:
LOCUS   AA264985       565 bp      mRNA           EST           27-NOV-1998
DEFINITION   LD08662.5prime LD Drosophila melanogaster embryo Bluescript
ACCESSION   AA264985
NID        92790170
VERSION    AA264985.1  GI:2790170
KEYWORDS    EST
SOURCE      fruit fly
ORGANISM    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 565)
AUTHORS     Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
            Brokstein,P., Lewis,S. and Rubin,G.M.
            BDGP/HMI Drosophila EST Project
            Unpublished (1997)
TITLE       On Jan 17, 1998 this sequence version replaced gi:1901019.
JOURNAL
COMMENT
FEATURES
    source
        1..565
            /organism="Drosophila melanogaster"
            /db_xref="BDGP_EST:BDc1n007993"
            /db_xref="taxon:7227"
            /clone_id="LD08662"
            /clone_lib="LD Drosophila melanogaster embryo Bluescript"
            /sex="male and female"
            /dev_stage="0 to 24 hours mixed stage embryonic"
            /lab_host="SOLR"
            /note="Organ: embryo; Vector: Bluescript SK; Site:1:
            EcoRI; Site:2: XhoI; Constructed using StrataGene ZAP-cDNA
            Synthesis kit. Oligo dt-primed and directionally cloned at
            EcoRI and XhoI in Bluescript SK(+/-)"
BASE COUNT   131 a      173 c      159 g      102 t
ORIGIN
alignment_scores:
    Quality:      75.00      Length:      28
    Ratio:        3.125      Gaps:      0
    Percent Similarity: 85.714      Percent Identity: 53.571
alignment_block:
US-08-699-716A-2 x AA264985 (3)  ..
Align seg 1/1 to: AA264985 from: 1 to: 565
2 GHHHHHHHHSSGHIDDDKMKRISS 29
||| |||||:||||:|:| |::
101 GHHGHHHHHTSANNVDGDTNKLPA 128
seq_name: gb_est25:A1260971
seq_documentation_block:
LOCUS   A1260971       572 bp      mRNA           EST           17-NOV-1998
DEFINITION   LP05026.5prime LP Drosophila melanogaster larval-early pupal
ACCESSION   A1260971
NID        93868496
VERSION    A1260971.1  GI:3868496
KEYWORDS    EST.

```

```

SOURCE      fruit fly.
ORGANISM    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 572)
AUTHORS     Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
            Brokstein,P., Lewis,S. and Rubin,G.M.
            BDGP/HMI Drosophila EST Project
            Unpublished (1997)
TITLE       On Aug 21, 1998 this sequence version replaced.
JOURNAL
COMMENT
FEATURES
    source
        1..572
            /organism="Drosophila melanogaster"
            /db_xref="taxon:7227"
            /clone="LP05026"
            /clone_lib="LP Drosophila melanogaster larval-early pupal
            pot2"
            /sex="male and female"
            /dev_stage="larvae-pupae"
            /lab_host="DH5-alpha"
            /note="Organ: whole body; Vector: pot2; Site:1: EcoRI;
            Site:2: XhoI; Sized fractionated cDNAs were directly
            ligated into pot2. Plasmid cDNA library."
BASE COUNT   132 a      174 c      162 g      104 t
ORIGIN
alignment_scores:
    Quality:      75.00      Length:      28
    Ratio:        3.125      Gaps:      0
    Percent Similarity: 85.714      Percent Identity: 53.571
alignment_block:
US-08-699-716A-2 x A1260971 (3)  ..
Align seg 1/1 to: A1260971 from: 1 to: 572
2 GHHHHHHHHSSGHIDDDKMKRISS 29
||| |||||:||||:|:| |::
100 GHHGHHHHHTSANNVDGDTNKLPA 127

```

11

OM of: us-08-699-716a-2 to: N_Geneseq_36.* out_format : pfs

Date: Nov 27, 1999 4:33 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-1998 Compugen Ltd.

Command line parameters:

-MODEL=sw.model -DEV=xldp
-Q=/cgn2.1/USPTO.spool/US08699716/runtat_27111999.151715.6614/app_query.fasta.1
-DB=N_Geneseq_36 -OPMT=fastap -SUFFIX=ring -GAPOP=11.000
-GAPEXT=11.000 -MINMATCH=0.100 -IOOPCL=0.000 -IOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -START=1 -DTRANS -MATRIX=pan150
-TRANS=human4.0.col -List=45 -DOCALIGN=200 -THR_SCORE=escore
-ALIGN=11 -MODE=LOCAL -OUTFMT=pfs -NORM=stat -USER=US08699716
-NCPU=6 -ICPU=3 -WAIT -DM_MEM=28000 -PM_MEM=15000 -THREADS=1

Search information block:

Query: US-08-699-716a-2
Query length: 521
Database: N_Geneseq_36.*
Database sequences: 311585
Database length: 125096042
Search time (sec): 73.360000

score list:

Sequence	Strid	Orig	ZScore	EScore	Len	Documentation
N_Geneseq_36:T38249	1	2111.00	5524.68	6.4e-300	1530	Y. pestis FI/V antigen gene 4
N_Geneseq_36:T38256	2	2029.00	5709.45	6.2e-288	1462	Y. pestis FI/V antigen gene 4
N_Geneseq_36:T04222	1	1443.00	3711.64	2.8e-202	1014	Y. pestis lcrv (V antigen) gene
N_Geneseq_36:T38242	1	1443.00	3711.64	2.8e-202	1014	Y. pestis lcrv (V antigen) gene
N_Geneseq_36:T38243	1	1443.00	3711.64	2.8e-202	1014	Y. pestis lcrv (V antigen) gene
N_Geneseq_36:T04223	1	1441.00	3766.38	5.5e-202	1014	Partial lcrv (V antigen) gene
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N_Geneseq_36:T092819	3	719.00	1873.72	1.5e-96	510	Yersinia pestis cati (F1) anti
N_Geneseq_36:T41594	2	719.00	1873.18	1.6e-96	544	Nucleotide sequence of FI anti
N_Geneseq_36:T41596	2	719.00	1873.18	1.6e-96	544	Nucleotide sequence of FI anti
N_Geneseq_36:T41609	1	634.00	1651.34	3.6e-84	447	Y. pestis FI antigen cati gene
N_Geneseq_36:T41601	1	634.00	1651.28	3.6e-84	450	Nucleotide sequence of FI anti
N_Geneseq_36:T41600	1	634.00	1650.80	3.8e-84	474	Nucleotide sequence of FI anti
N_Geneseq_36:T092817	2	633.00	1644.46	8.6e-84	541	Yersinia pestis cati (F1) anti
N_Geneseq_36:T38244	2	633.00	1644.46	8.6e-84	541	Y. pestis cati (F1 antigen) ge
N_Geneseq_36:T092818	3	631.00	1641.83	1.2e-83	542	Yersinia pestis cati (F1) anti
N_Geneseq_36:T41558	1	571.00	1483.50	8.0e-75	576	Nucleotide sequence of FI anti
N_Geneseq_36:T41559	1	486.00	1260.98	2.0e-62	513	Nucleotide sequence of FI anti
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N_Geneseq_36:T45347	1	120.00	294.10	1.4e-08	861	Single chain sfv anti-rev anti
N_Geneseq_36:T54056	2	113.00	282.90	6.0e-08	375	DNA fragment 2 of the wild tyf
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155 GGLAGKAGKTYTDAVTYVSNQSGIEGRIRAYEQNPQHIEDLEKRYVEQJLT 204
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221 GGGSSVLEELVOLVKDKNIDISIKYDPKDEVFANRVITDDIELLKKIL 270
|||||
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271 AYFLPEDTILKGGHYDNOLONGIKRYVEFLSSPNTOWELRAFMAVMHFS 320
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255 AYFLPEDALIKGGHYDNOLONGIKRYVEFLSSPNTOWELRAFMAVMHFS 304
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321 LTADRIDDILKVIYDSMNHGDARSKLRELAELAEIKIYVIOAEIN 370
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371 KHLSSGTINIHDKSINLMDKNLYGTDEEFKASAEYKLEKMPOTTTIO 420
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421 VDGESEKRIYSIKDFLGESENKRTGALGNLKNYSYNKDNNELSHFATTCSD 470
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521 K 521
|
505 K 505

seq_name: N_Geneseq_36:T38256

seq_documentation_block:
ID T38256 standard: DNA: 1462 BP.
AC T38256.
DT 28-DEC-1996 (first entry)
DE Y. pestis F1/V antigen gene fusion.
KW Plaque; vaccine; genetic immunisation; V antigen; lcrV;
KW F1 antigen; caf1; ds.
OS Chimeric Yersinia pestis strain GB;
OS Chimeric synthetic.
FH Key Location/Qualifiers
FT cds 8..1450
FT /tag= a
FT /product= F1/V fusion protein
FT misc_feature 452..472
FT /tag= b
FT /note= "bases 452-472 is a sequence derived
FT from PCR primers"
PD WO9628551-A1.
PF 19-SEP-1996.
PF 13-MAR-1996; G00571.
PR 13-MAR-1995; GB-005059.
PR 13-SEP-1995; GB-018946.
PR 05-DEC-1995; GB-024825.
PA (MINA ) UK SEC FOR DEFENCE.
PI Bennett AM, leary SEC, Oyston PCF, Titball RW, Williamson ED;
DR WPT: 96-433824/43.
P-PSDB: W01045.
DT Yersinia pestis V antigen and F1 antigen or their protective
PT epitopic parts - useful in vaccine for protection against plague
PS Disclosure: Page 51-55; 98pp; English.
CC A gene fusion (T38256) comprises coding sequences for the Yersinia
CC pestis F1 antigen (see also T38244) (without the signal sequence)
CC and for the Y. pestis V antigen (see also T38243), joined by a
CC sequence encoding a 6-amino acid peptide linker. It was obt. by
CC PCR amplification of the individual genes using primers (see also
CC T38245) based on the genes and including linker sequences. The
CC gene fusion (see also T38249) can be used to produce F1/V fusion
CC protein (W01045) in transformed cells, esp. gut-colonising
```

```
CC organisms, to induce an immune response against Y. pestis, the
CC causative organism of plague.
SQ Sequence 1462 BP: 476 A; 285 C; 301 G; 400 T;

alignment_scores:
Quality: 2029.00 Length: 482
Ratio: 4.254 Gaps: 1
Percent Similarity: 98.963 Percent Identity: 98.133

alignment_block:
US-08-699-716a-2 x T38256 (2) ..

Align seg 1/1 to: T38256 from: 1 to: 1462

43 NADLTASTATATATLEPARITLTYKEGAPITIMDNGNIDELLYGTLT 92
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1 LSADLJASTATATATLEPARITLTYKEGAPITIMDNGNIDELLYGTLT 50
93 GGYKTGTSTSYNFTDAGDPMYLTFTSODGNNHOTTVKVIGKDSRDEI 142
51 GGYKTGTSTSYNFTDAGDPMYLTFTSODGNNHOTTVKVIGKDSRDEI 100
143 SPRKNGENLVGDVYLVATGSDPEFVRSIGSKGKTLAAGKYTDAVTYVSN 192
101 SPRKNGENLVGDVYLVATGSDPEFVRSIGSKGKTLAAGKYTDAVTYVSN 150
193 Q...EFMIRAYEQNPQHIEDLEKRYVEQJLTGSSVLEELVOLVKDKNI 239
151 QGSIEGRIRAYEQNPQHIEDLEKRYVEQJLTGSSVLEELVOLVKDKNI 200
240 DISIKYDPKDEVFANRVITDDIELLKKILAYFLPEDTILKGGHYDNL 289
201 DISIKYDPKDEVFANRVITDDIELLKKILAYFLPEDALIKGGHYDNL 250
290 ONGIKRYVEFLSSPNTOWELRAFMAVMHFSLTADRIDDILKVIYDSMN 339
251 ONGIKRYVEFLSSPNTOWELRAFMAVMHFSLTADRIDDILKVIYDSMN 300
340 HGGDARSKLRELAELAEIKIYVIOAEINKHLSSSGTINIHDKSINIM 389
301 HGGDARSKLRELAELAEIKIYVIOAEINKHLSSSGTINIHDKSINIM 350
390 DKNLYGTDEEFKASAEYKILEKMPOTTIOVDGESEKRIYSIKDFLGSN 439
351 DKNLYGTDEEFKASAEYKILEKMPOTTIOVDGESEKRIYSIKDFLGSN 400
440 KRTGALGNLKNYSYNKDNNELSHFATTCSDKSRPLDLVSOQKTQJLSDI 489
401 KRTGALGNLKNYSYNKDNNELSHFATTCSDKSRPLDLVSOQKTQJLSDI 450
490 TSRFNSAIEALNRITQKYDSVMORLDDTSGK 521
451 TSRFNSAIEALNRITQKYDSVMORLDDTSGK 482

seq_name: N_Geneseq_36:T04222

seq_documentation_block:
ID T04222 standard: DNA: 1014 BP.
AC T04222.
DT 18-APR-1996 (first entry)
DE Partial lcrV (V antigen) gene of Y. pestis.
KW lcrV; V antigen; virulence; plaque; vaccine; epitope; ss.
OS Yersinia pestis.
FH Key Location/Qualifiers
FT cds 1..990
FT /tag= a
FT /note= "V antigen"
PD WO9524475-A1.
PF 14-SEP-1995.
PF 06-MAR-1995; G00481.
PR 08-MAR-1994; GB-004577.
PA (MINA ) UK SEC FOR DEFENCE.
```

```
PI Leary SEC, Titball RM, Williamson ED, Leary SE;
DR WPI:95-328268/42.
P-PSDB: R/9961.
PT Recombinant DNA expressing Yersinia pestis V antigen - useful in
PT oral or parenteral vaccines for protection against plague
PS Claim 6: Page 11-13: 25pp: English.
CC T04222-23 are DNA sequences (lcrV) encoding all or a protective epitopic
CC part of the mature V protein of Yersinia pestis. The protein was
CC expressed as a fusion protein with maltose binding protein or
CC glutathione-S-transferase in 3 different plasmid vectors. Y. pestis is
CC the highly virulent causative organism of plague in a wide range of
CC animals, including man. The V antigen (lcrV) is an unstable 37.3 kDa
CC monomeric peptide encoded on the ca. 70 kb lcr plasmid. The V antigen
CC is postulated to act as a virulence antigen, and transformed
CC microorganisms contg. recombinant DNA encoding a V antigen protein/
CC peptide are useful in vaccines to protect against plague.
SQ Sequence 1014 BP; 346 A; 181 C; 201 G; 286 T;

alignment_scores:
Quality: 1443.00 Length: 325
Ratio: 4.440 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.692

alignment_block:
US-08-699-716a-2 x T04222 (1) ..
Align seg 1/1 to: T04222 from: 1 to: 1014

197 IRAYEONPOHFIEDLEKVRVEQOLTGHGSSVLEELVOLVKKNIDISIKYD 246
|||||
5 IRAYEONPOHFIEDLEKVRVEQOLTGHGSSVLEELVOLVKKNIDISIKYD 54
247 PRDSEVFARVITDDIELLKKILAYFLPEDTILKGGHYNOQNGIKRV 296
|||||
55 PRDSEVFARVITDDIELLKKILAYFLPEDAILKGGHYNOQNGIKRV 104
297 KEFLSSPNTQWELRAFMAVMHFSLTADRIDDDILKVIYDSMNHGDARS 346
|||||
105 KEFLSSPNTQWELRAFMAVMHFSLTADRIDDDILKVIYDSMNHGDARS 154
347 KLREBELAELTAEIKIYSVIOAEINKHLSSSGTINIHDKSINLMDKNLYGY 396
|||||
155 KLREBELAELTAEIKIYSVIOAEINKHLSSSGTINIHDKSINLMDKNLYGY 204
397 TDEIFRASAERYKILEKMPOTTIOVDSSEKKIYSIKDFLSENNKRTGALG 446
|||||
205 TDEIFRASAERYKILEKMPOTTIOVDSSEKKIYSIKDFLSENNKRTGALG 254
447 NLKNSYSYNKDNNELSHFATTCSDKSRPLNDIVSOQTTOLSDITSRFNSA 496
|||||
255 NLKNSYSYNKDNNELSHFATTCSDKSRPLNDIVSOQTTOLSDITSRFNSA 304
497 IEALNRFIOKYDSVMORLLDDTSGK 521
|||||
305 IEALNRFIOKYDSVMORLLDDTSGK 329

seq_name: N_Geneseq_36:T38242

seq_documentation_block:
ID T38242 standard; DNA: 1014 BP.
AC T38242;
DE 28-DEC-1996 (first entry)
KW Y. pestis lcrV (V antigen) gene.
KW Plague; vaccine; genetic immunisation; V antigen; lcrV;
OS Yersinia pestis strain GB.
FH key Location/Qualifiers
FT cds 1..990
FT misc-feature 1..6
FT FT /*tag= a
FT FT /*tag= b
FT FT /note= "vector pMAL-p2 or pMAL-c2-derived bases"
```

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FT mutation 1006
FT FT /*tag= c
FT FT /note= "base 1006 is altered to a T to create a
FT FT second in-frame stop codon"
PN WO9628551-A1.
PR 19-SEP-1996.
PP 13-MAR-1996; G00571.
PR 13-MAR-1995; GB-0050509.
PR 15-SEP-1995; GB-018946.
PR 05-DEC-1995; GB-024825.
PA (MINA) UK SEC FOR DEFENCE.
PI Bennett AM, Leary SEC, Oyston PCF, Titball RM, Williamson ED;
DR WPI:96-433824/43.
P-PSDB: W01040.
PT Yersinia pestis V antigen and F1 antigen or their protective
PT epitopic parts - useful in vaccine for protection against plague
PS Claim 5: Page 25-28: 98pp: English.
CC A lcrV gene sequence (T38242) codes for the Yersinia pestis V
CC antigen (W01040), which is capable of evoking protective immune
CC responses in animals. The gene was amplified from Y. pestis
CC DNA by PCR using primers (T38250-51) homologous to the 5' and 3'
CC ends of the gene. The gene was inserted into vector pMAL-p2,
CC pMAL-c2 or pGEX-5x-2 (see also T38243) to allow prodn. of
CC recombinant V antigen for use in vaccines against plague.
CC Expression in gut-colonising organisms and attenuated Salmonella
CC typhi allows prodn. of live vaccines. F1/V antigen fusions were
CC also created (see also T38249 and T38256). The gene can itself be
CC used in genetic vaccines.
SQ Sequence 1014 BP; 347 A; 180 C; 201 G; 286 T;
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alignment_scores:
Quality: 1443.00 Length: 325
Ratio: 4.440 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.692

alignment_block:
US-08-699-716a-2 x T38242 (1) ..
Align seg 1/1 to: T38242 from: 1 to: 1014

197 IRAYEONPOHFIEDLEKVRVEQOLTGHGSSVLEELVOLVKKNIDISIKYD 246
|||||
5 IRAYEONPOHFIEDLEKVRVEQOLTGHGSSVLEELVOLVKKNIDISIKYD 54
247 PRDSEVFARVITDDIELLKKILAYFLPEDTILKGGHYNOQNGIKRV 296
|||||
55 PRDSEVFARVITDDIELLKKILAYFLPEDAILKGGHYNOQNGIKRV 104
297 KEFLSSPNTQWELRAFMAVMHFSLTADRIDDDILKVIYDSMNHGDARS 346
|||||
105 KEFLSSPNTQWELRAFMAVMHFSLTADRIDDDILKVIYDSMNHGDARS 154
347 KLREBELAELTAEIKIYSVIOAEINKHLSSSGTINIHDKSINLMDKNLYGY 396
|||||
155 KLREBELAELTAEIKIYSVIOAEINKHLSSSGTINIHDKSINLMDKNLYGY 204
397 TDEIFRASAERYKILEKMPOTTIOVDSSEKKIYSIKDFLSENNKRTGALG 446
|||||
205 TDEIFRASAERYKILEKMPOTTIOVDSSEKKIYSIKDFLSENNKRTGALG 254
447 NLKNSYSYNKDNNELSHFATTCSDKSRPLNDIVSOQTTOLSDITSRFNSA 496
|||||
255 NLKNSYSYNKDNNELSHFATTCSDKSRPLNDIVSOQTTOLSDITSRFNSA 304
497 IEALNRFIOKYDSVMORLLDDTSGK 521
|||||
305 IEALNRFIOKYDSVMORLLDDTSGK 329

seq_name: N_Geneseq_36:T38243

seq_documentation_block:
ID T38243 standard; DNA: 1014 BP.
```

```
AC T38243:
DE 28-DEC-1996 (first entry)
DE Y. pestis lcrV (V antigen) gene.
KW Plaque; vaccine; genetic immunisation; V antigen; lcrV;
KW Fl antigen; ds.
OS Yersinia pestis strain GB.
FH Key location/Qualifiers
FT cds 1..990
FT misc-feature /*tag= a
FT /*tag= 1..10
FT /*tag= b
FT /*note= "vector pGEX-5X-2-derived bases"
FT mutation 16
FT /*tag= c
FT /*note= "base 16 is altered to a C from an
FT A to createan EcoRI site"
FT mutation 1006
FT /*tag= d
FT /*note= "base 1006 is altered to a T to create a
FT second in-frame stop codon"
PN W09628551-A1.
PD 19-SEP-1996.
PF 13-MAR-1996; G00571.
PR 13-MAR-1995; GB-005059.
PR 15-SEP-1995; GB-018946.
PR 05-DEC-1995; GB-024825.
PA (MINA ) UK SEC FOR DEFENCE.
PI Bennett AM, Leary SEC, Oyston PCF, Titball RW, Williamson ED;
DR WPI; 96-433824/43.
DR P-PSDB: W01041.
PT Yersinia pestis V antigen and Fl antigen or their protective
PT epitopic parts - useful in vaccine for protection against plague
CC Claim 5: Page 32-35; 98pp; English.
CC A lcrV gene sequence (T38243) codes for the Yersinia pestis V
CC antigen (W01041), which is capable of evoking protective immune
CC responses in animals. The gene was amplified from Y. pestis
CC DNA by PCR using primers (T38251 and T38259) homologous to the 5'
CC and 3' ends of the gene. The gene was inserted into vector
CC pEX-5X-2, PMAL-p2 or PMAL-c2 (see also T38242) to allow prodn. of
CC recombinant V antigen for use in vaccines against plague.
CC Expression in gut-colonising organisms and attenuated Salmonella
CC typhi allows live vaccine prodn. Fl/V antigen fusions were also
CC created (see also T38249 and T38256). The gene can itself be used
CC in genetic vaccines.
SQ Sequence 1014 BP; 343 A; 184 C; 205 G; 282 T;

alignment_scores:
Quality: 1443.00 Length: 325
Ratio: 4.440 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.692

alignment_block:
US-08-699-716A-2 x T38243 (1) ..
Align seg 1/1 to: T38243 from: 1 to: 1014

197 IRAYEONPOHFIEDELEKRVVEOLTGHGSSVLEELVOLVKDKNIDISTKYD 246
|||||
5 IRAYEONPOHFIEDELEKRVVEOLTGHGSSVLEELVOLVKDKNIDISTKYD 54
247 PRKDSVEFANRVITDDIELKKILAYFLPEPTILKGGHYDNLONGIKRV 296
|||||
55 PRKDSVEFANRVITDDIELKKILAYFLPEPTILKGGHYDNLONGIKRV 104
297 KEFLSSPNTQWELRAEFAVMHFSLTADRIDDLIKYIVDSMNHGARS 346
|||||
105 KEFLSSPNTQWELRAEFAVMHFSLTADRIDDLIKYIVDSMNHGARS 154
347 KLREELATLAEIKIYSYIOAEINKHLSSTGTINIHDSINIMDKNLXGY 396
|||||
155 KLREELATLAEIKIYSYIOAEINKHLSSTGTINIHDSINIMDKNLXGY 204
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397 TDEEFKASAEYKILIEKMPOTTIOVDSEKRIYVSKDFLSENRKTALG 446
|||||
205 TDEEFKASAEYKILIEKMPOTTIOVDSEKRIYVSKDFLSENRKTALG 254
447 NLKNSYSYKNNNELSHFATCSDKSRPLNDVSOQTOLSDISRFNSA 496
|||||
255 NLKNSYSYKNNNELSHFATCSDKSRPLNDVSOQTOLSDISRFNSA 304
497 IEALNRFIOKYDSVMORLLDPTSGK 521
|||||
305 IEALNRFIOKYDSVMORLLDPTSGK 329

seq_name: N_Geneseq_36:T04223

seq_documentation_block:
ID T04223 standard; DNA; 1014 BP.
AC T04223;
DE 18-APR-1996 (first entry)
DE Partial lcrV (V antigen) gene of Y. pestis.
KW lcrV; V antigen; virulence; plaque; vaccine; epitope; ss.
OS Yersinia pestis.
FH Key location/Qualifiers
FT cds 1..990
FT /*tag= a
PN W09524475-A1.
PD 14-SEP-1995.
PF 06-MAR-1995; G00481.
PR 08-MAR-1994; GB-004577.
PA (MINA ) UK SEC FOR DEFENCE.
PI Leary SEC, Titball RW, Williamson ED, Leary SE;
DR WPI; 95-328268/42.
DR P-PSDB: R79962.
PT Recombinant DNA expressing Yersinia pestis V antigen - useful in
PT oral or parenteral vaccines for protection against plague
PS Claim 6: Page 15-16; 25pp; English.
CC T04222-23 are DNA sequences (lcrV) encoding all or a protective epitopic
CC part of the mature V protein of Yersinia pestis. The protein was
CC expressed as a fusion protein with maltose binding protein or
CC glutathione-S-transferase in 3 different plasmid vectors. Y. pestis
CC is the highly virulent causative organism of plague in a wide range of
CC animals, including man. The V antigen (lcrV) is an unstable 37.3 kDa
CC monomeric peptide encoded on the ca. 70 kb lcr plasmid. The V antigen
CC is postulated to act as a virulence antigen, and transformed
CC microorganisms contg. recombinant DNA encoding a V antigen protein/
CC peptide are useful in vaccines to protect against plague.
SQ Sequence 1014 BP; 343 A; 185 C; 204 G; 282 T;

alignment_scores:
Quality: 1441.00 Length: 325
Ratio: 4.434 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.385

alignment_block:
US-08-699-716A-2 x T04223 (1) ..
Align seg 1/1 to: T04223 from: 1 to: 1014

197 IRAYEONPOHFIEDELEKRVVEOLTGHGSSVLEELVOLVKDKNIDISTKYD 246
|||||
5 IRAYEONPOHFIEDELEKRVVEOLTGHGSSVLEELVOLVKDKNIDISTKYD 54
247 PRKDSVEFANRVITDDIELKKILAYFLPEPTILKGGHYDNLONGIKRV 296
|||||
55 PRKDSVEFANRVITDDIELKKILAYFLPEPTILKGGHYDNLONGIKRV 104
297 KEFLSSPNTQWELRAEFAVMHFSLTADRIDDLIKYIVDSMNHGARS 346
|||||
105 KEFLSSPNTQWELRAEFAVMHFSLTADRIDDLIKYIVDSMNHGARS 154
347 KLREELATLAEIKIYSYIOAEINKHLSSTGTINIHDSINIMDKNLXGY 396
|||||
155 KLREELATLAEIKIYSYIOAEINKHLSSTGTINIHDSINIMDKNLXGY 204
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397 TDEEIFKAAEYKILEKMPÖTTIÖVDGSEKKIYSIKDFJGSEKKRTGALG 446
|||||
205 TDEEIFKAAEYKILEKMPÖTTIÖVDGSEKKIYSIKDFJGSEKKRTGALG 254
|||||
447 NIKNSYSYKKNDELSEFAITCSDKSRPLNDLVSOQTOTLOLSDTSFNRA 496
|||||
255 NIKNSISTYKKNDELSEFAITCSDKSRPLNDLVSOQTOTLOLSDTSFNRA 304
|||||
497 IEALNRFIOKYDSVMÖRLDDTSGK 521
|||||
305 IEALNRFIOKYDSVMÖRLDDTSGK 329
|||||

seq_name: N_Geneseq_36:V41595

seq_documentation_block:
ID V41595 standard: DNA: 510 BP.
AC V41595:
DE 26-OCT-1998 (first entry)
DT Nucleotide sequence of F1 antigen nypfl(b)sec544.
PS F1 antigen: plasmid; vaccine; plague; ds.
OS Yersinia pestis.
PN WO9824912-A2.
PD 11-JUN-1998:
PF 04-DEC-1997: U22617.
PR 04-DEC-1996: US-767115.
PA (HESK-) HESKA CORP.
PI Haanes EJ, Osorio JE, Thomas RE;
DR WPI: 98-333331/29.
PT Protection of animals against plague - using nucleic acid encoding
PT antigen from Yersinia, Pasteurella and Francisella spp.
CC This is the nucleotide sequence of a Yersinia pestis F1 antigen, used
CC in the method of the invention. Plasmid and host cells are used to
CC produce recombinant antigens, especially Yersinia pestis antigens.
CC The recombinant antigens can be used in vaccines that are capable of
CC protecting an animal from contracting plague.
SQ Sequence 510 BP; 153 A; 114 C; 106 G; 137 T;

alignment_scores:
Quality: 719.00 Length: 170
Ratio: 4.229 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-699-716a-2 x V41595 (1) ..

Align seg 1/1 to: V41595 from: 1 to: 510

24 MKKISSVIAIALFGTATANAADLTASTATATVLEPARITLYKEGAPI 73
|||||
1 MKKISSVIAIALFGTATANAADLTASTATATVLEPARITLYKEGAPI 50
|||||
74 TIMDNGNIDTELLVGTITLGKYGKGTSTSVNFTDAAGPMLTFTSODG 123
|||||
51 TIMDNGNIDTELLVGTITLGKYGKGTSTSVNFTDAAGPMLTFTSODG 100
|||||
124 NNHÖFTTKVIGKDSRDFDISPKVNGENLVGDVYLATGSDPFFVRSISGK 173
|||||
101 NNHÖFTTKVIGKDSRDFDISPKVNGENLVGDVYLATGSDPFFVRSISGK 150
|||||
174 GGLAAGKYTDAVTVVSNÖ 193
|||||
151 GGLAAGKYTDAVTVVSNÖ 170
|||||

seq_name: N_Geneseq_36:Q92819

seq_documentation_block:
ID Q92819 standard: DNA: 542 BP.
AC Q92819:
DT 17-DEC-1995 (first entry)
DT Yersinia pestis cafl (F1) antigen in plasmid pFORF1b.

KW Vaccine; antigen: Salmonella typhimurium; Salmonella typhi;
KW bubonic plague; pneumonic plague; ds.
OS Yersinia pestis.
FH Key Location/Qualifiers
FT cds 2..7
FT /*tag= a
FT /note= "first protein encoded by pFORF1b"
FT misc_feature 1..6
FT /*tag= b
FT misc_feature 536..541
FT /*tag= c
FT /note= "cafl open reading frame downstream seq."
FT cds 21..530
FT /*tag= d
FT /note= "cafl fusion protein"

WO9518231-A1.
PD 06-JUL-1995.
PF 23-DEC-1994: G02818.
PR 24-DEC-1993: GB-026425.
PA (MINA) UK SEC FOR DEFENCE.
PI Howells A, Leary SEC, Oyston PCF, Titball RW, Williamson ED;
DR P-PSDB: R76528.
PT DNA constructs capable of transforming microorganisms - which can be
PT used as live or attenuated vaccines which induce an immune response,
PT against Yersinia pestis, at mucosal surfaces.
PS Disclosure: Page 19-20: 27pp: English.
CC The sequence represents the plasmid pFORF1b including the entire
CC Y. pestis cafl (F1) antigen gene having a 5' tail including a SacI
CC restriction site, and up to TATAG downstream of the cafl ORF.
CC The DNA construct can be used to transform human or animal gut
CC colonizing microorganisms, specifically attenuated Salmonella
CC typhimurium or Salmonella typhi. The transformed microorganisms
CC can be used as live/attenuated vaccines which induce immune
CC responses at mucosal surfaces. The vaccines provide protection
CC against infection with Y. pestis, and are parenterally and orally
CC active vaccines offering protection against bubonic and pneumonic
CC plague.
SQ Sequence 542 BP; 164 A; 118 C; 114 G; 146 T;

alignment_scores:
Quality: 719.00 Length: 170
Ratio: 4.229 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-699-716a-2 x Q92819 (3) ..

Align seg 1/1 to: Q92819 from: 1 to: 542

24 MKKISSVIAIALFGTATANAADLTASTATATVLEPARITLYKEGAPI 73
|||||
7 MKKISSVIAIALFGTATANAADLTASTATATVLEPARITLYKEGAPI 56
|||||
74 TIMDNGNIDTELLVGTITLGKYGKGTSTSVNFTDAAGPMLTFTSODG 123
|||||
57 TIMDNGNIDTELLVGTITLGKYGKGTSTSVNFTDAAGPMLTFTSODG 106
|||||
124 NNHÖFTTKVIGKDSRDFDISPKVNGENLVGDVYLATGSDPFFVRSISGK 173
|||||
107 NNHÖFTTKVIGKDSRDFDISPKVNGENLVGDVYLATGSDPFFVRSISGK 156
|||||
174 GGLAAGKYTDAVTVVSNÖ 193
|||||
157 GGLAAGKYTDAVTVVSNÖ 176
|||||

seq_name: N_Geneseq_36:V41594

seq_documentation_block:
ID V41594 standard: DNA: 544 BP.
AC V41594:
DT 26-OCT-1998 (first entry)

```
DE Nucleotide sequence of F1 antigen nypF1(a)sec544.
KW F1 antigen; plasmid; vaccine; plaque; ds.
OS Yersinia pestis.
FH Key Location/Qualifiers
FT CDS 17..529
FT     /tag= a
FT     /product= "F1 antigen"
PN WO9824912-A2.
PD 11-JUN-1998.
PE 04-DEC-1997; U22617.
PR 04-DEC-1996; US-767115.
PA (HESK-) HESKA CORP.
PI Haanes EJ, Osorio JE, Thomas RE;
DR WPI: 98-333331/29.
DR P-PSDB: W59782.
PT Protection of animals against plague - using nucleic acid encoding
  antigen from Yersinia, Pasteurella and Francisella spp.
PS Claim 8; Page 51; 75pp; English.
CC This is the nucleotide sequence of a Yersinia pestis F1 antigen, used
  in the method of the invention. Plasmid and host cells are used to
  produce recombinant antigens, especially Yersinia pestis antigens.
  The recombinant antigens can be used in vaccines that are capable of
  protecting an animal from contracting plague.
CC
SQ Sequence 544 BP; 164 A; 120 C; 114 G; 146 T;

alignment_scores:
  Quality: 719.00      Length: 170
  Ratio: 4.229        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-08-699-716a-2 x V41594 (2) ..
Align seg 1/1 to: V41594 from: 1 to: 544

24 MKKISSVIAALFGTATATANAADLTASTATATATLVEPARITLYKKGAPI 73
   |||||||||||||||||||||||||||||||||||||||||||||||||||
   6 MKKISSVIAALFGTATATANAADLTASTATATLVEPARITLYKKGAPI 55
   |||||||||||||||||||||||||||||||||||||||||||||||||||
74 TIMDNGNIDTELLVGTLLTGGYKKTGTTSTSVNFTDAAGDPMYLFTFSQDG 123
   |||||||||||||||||||||||||||||||||||||||||||||||||||
56 TIMDNGNIDTELLVGTLLTGGYKKTGTTSTSVNFTDAAGDPMYLFTFSQDG 105
   |||||||||||||||||||||||||||||||||||||||||||||||||||
124 NNHQFTKVIKDSRDEDISPKVNGENLVGDVYLATGSDQDFVRSIGSK 173
   |||||||||||||||||||||||||||||||||||||||||||||||||||
106 NNHQFTKVIKDSRDEDISPKVNGENLVGDVYLATGSDQDFVRSIGSK 155
   |||||||||||||||||||||||||||||||||||||||||||||||||||
174 GCKLAGKXTDAVTYVSNO 193
   |||||||||||||||||||||||||||||||||||||||||||||||||||
156 GCKLAGKXTDAVTYVSNO 175
   |||||||||||||||||||||||||||||||||||||||||||||||||||

seq_name: N_Geneseq_36:V41596

seq_documentation_block:
ID V41596 standard: DNA: 544 BP.
AC V41596.
DT 26-OCT-1998 (first entry)
DE Nucleotide sequence of F1 antigen nypF1sec510.
KW F1 antigen; plasmid; vaccine; plaque; ds.
OS Yersinia pestis.
FH Key Location/Qualifiers
FT CDS 17..532
FT     /tag= a
FT     /product= "F1 antigen"
PN WO9824912-A2.
PD 11-JUN-1998.
PE 04-DEC-1997; U22617.
PR 04-DEC-1996; US-767115.
PA (HESK-) HESKA CORP.
PI Haanes EJ, Osorio JE, Thomas RE;
DR WPI: 98-333331/29.
DR P-PSDB: W59783.
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PT Protection of animals against plague - using nucleic acid encoding
  antigen from Yersinia, Pasteurella and Francisella spp.
PS Claim 8; Pages 53-54; 75pp; English.
CC This is the nucleotide sequence of a Yersinia pestis F1 antigen, used
  in the method of the invention. Plasmid and host cells are used to
  produce recombinant antigens, especially Yersinia pestis antigens.
  The recombinant antigens can be used in vaccines that are capable of
  protecting an animal from contracting plague.
CC
SQ Sequence 544 BP; 166 A; 118 C; 112 G; 148 T;

alignment_scores:
  Quality: 719.00      Length: 170
  Ratio: 4.229        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-08-699-716a-2 x V41596 (2) ..
Align seg 1/1 to: V41596 from: 1 to: 544

24 MKKISSVIAALFGTATATANAADLTASTATATLVEPARITLYKKGAPI 73
   |||||||||||||||||||||||||||||||||||||||||||||||||||
   6 MKKISSVIAALFGTATATANAADLTASTATATLVEPARITLYKKGAPI 55
   |||||||||||||||||||||||||||||||||||||||||||||||||||
74 TIMDNGNIDTELLVGTLLTGGYKKTGTTSTSVNFTDAAGDPMYLFTFSQDG 123
   |||||||||||||||||||||||||||||||||||||||||||||||||||
56 TIMDNGNIDTELLVGTLLTGGYKKTGTTSTSVNFTDAAGDPMYLFTFSQDG 105
   |||||||||||||||||||||||||||||||||||||||||||||||||||
124 NNHQFTKVIKDSRDEDISPKVNGENLVGDVYLATGSDQDFVRSIGSK 173
   |||||||||||||||||||||||||||||||||||||||||||||||||||
106 NNHQFTKVIKDSRDEDISPKVNGENLVGDVYLATGSDQDFVRSIGSK 155
   |||||||||||||||||||||||||||||||||||||||||||||||||||
174 GCKLAGKXTDAVTYVSNO 193
   |||||||||||||||||||||||||||||||||||||||||||||||||||
156 GCKLAGKXTDAVTYVSNO 175
   |||||||||||||||||||||||||||||||||||||||||||||||||||

seq_name: N_Geneseq_36:T38248

seq_documentation_block:
ID T38248 standard: DNA: 547 BP.
AC T38248.
DT 28-DEC-1996 (first entry)
DE Y. pestis F1 antigen cafI gene (including signal sequence).
KW Plaque; vaccine; genetic immunisation; F1 antigen; cafI;
  V antigen; ds.
OS Yersinia pestis strain GB.
FH Key Location/Qualifiers
FT signal_peptide 29..91
FT     /tag= a
FT     /product= b
FT mat_peptide 92..538
FT     /tag= b
PN WO9628551-A1.
PD 19-SEP-1996.
PE 13-MAR-1996; G00571.
PR 13-MAR-1995; GB-005059.
PR 15-SEP-1995; GB-018946.
PR 05-DEC-1995; GB-024825.
PA (MINA ) UK SEC FOR DEFENCE.
PI Bennett AM, Leary SEC, Oyston PCF, Titball RW, Williamson ED;
DR WPI: 96-433824/43.
DR P-PSDB: W01043.
PT Yersinia pestis V antigen and F1 antigen or their protective
  epitopic parts - useful in vaccine for protection against plague
PS Claim 41; Page 61-62; 98pp; English.
CC A DNA sequence (T38248) comprises the cafI gene, including the
  signal sequence, coding for the F1 antigen (W01043) of Yersinia
  pestis. It was obtd. by PCR amplification (see also T38257-58)
  of Y. pestis DNA. The PCR product was cloned into plasmid pBKCMV
  and the resulting plasmid (pT38248) was used to transform E. coli Nova
  Blue. Purified plasmid, when administered by i.m. injection,
  induced an immunoglobulin response to F1 in BalB/c mice. Live
  vaccines comprising gut colonising organisms transformed with the
```

CC cagl gene (see also T38244) can be used to protect a host animal
CC against plague.
SQ Sequence 547 BP; 165 A; 120 C; 115 G; 147 T;

alignment_scores:
Quality: 719.00 Length: 170
Ratio: 4.229 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-699-716A-2 x T38248 (2)

Align seg 1/1 to: T38248 from: 1 to: 547

```
24 MKKISSVIAIPLFGITATANADLTATATATVEPARITLYKEGAPI 73
|||||
10 MKKISSVIAIPLFGITATANADLTATATATVEPARITLYKEGAPI 59
74 TIMDNGNIDTELVGTLTGKGTGTSTSVNFTDAAGDPMYLFTTSODG 123
|||||
60 TIMDNGNIDTELVGTLTGKGTGTSTSVNFTDAAGDPMYLFTTSODG 109
124 NNHOFTRKVIKDSRDEISPKVNGENLVGDVVLATGSQDFEVRISIGSK 173
|||||
110 NNHOFTRKVIKDSRDEISPKVNGENLVGDVVLATGSQDFEVRISIGSK 159
174 GSKLAAGKYTDAVTVTVSNQ 193
|||||
160 GSKLAAGKYTDAVTVTVSNQ 179
```

seq_name: N_Geneseq_36:V41609

seq_documentation_block:

ID V41609 standard; DNA: 447 BP.
AC V41609;
DT 26-OCT-1998 (first entry)
DE Nucleotide sequence of F1 antigen nyfpmat447.
KW F1 antigen; plasmid; vaccine; plague; ds.
OS Yersinia pestis.
FH Key Location/Qualifiers
FT CDS 1..447
FT /tag= a
FT /product= "F1 antigen"
PN MO9824912-A2.
PD 11-JUN-1998.
PE 04-DEC-1997; 022617.
PR 04-DEC-1996; US-767115.
PA (HESK-) HESKA CORP.
PI Haanes EJ, Osorio JE, Thomas RE;
DR P-PSDB: W59788.
PT Protection of animals against plague - using nucleic acid encoding
PT antigen from Yersinia, Pasteurella and Francisella spp.
PS Claim 8; Page 64; 75pp; English.
CC This is the nucleotide sequence of a Yersinia pestis F1 antigen, used
CC in the method of the invention. Plasmid and host cells are used to
CC produce recombinant antigens, especially Yersinia pestis antigens.
CC The recombinant antigens can be used in vaccines that are capable of
CC protecting an animal from contracting plague.
SQ Sequence 447 BP; 133 A; 102 C; 95 G; 117 T;

alignment_scores:
Quality: 634.00 Length: 149
Ratio: 4.255 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-699-716A-2 x V41609 (1)
Align seg 1/1 to: V41609 from: 1 to: 447

```
45 ADLTAATATATVEPARITLYKEGAPITIMDNGNIDTELVGTLTGG 94
|||||
1 ADLTAATATATVEPARITLYKEGAPITIMDNGNIDTELVGTLTGG 50
95 YKGTGTSTSVNFTDAAGDPMYLFTTSODGNNHOTTYVIGKDSRDEISP 144
|||||
51 YKGTGTSTSVNFTDAAGDPMYLFTTSODGNNHOTTYVIGKDSRDEISP 100
145 KVNGENLVGDVVLATGSQDFEVRISIGSKGKLAAGKYTDAVTVTVSNQ 193
|||||
101 KVNGENLVGDVVLATGSQDFEVRISIGSKGKLAAGKYTDAVTVTVSNQ 149
```

seq_name: N_Geneseq_36:V41601

seq_documentation_block:

ID V41601 standard; DNA: 450 BP.
AC V41601;
DT 26-OCT-1998 (first entry)
DE Nucleotide sequence of F1 antigen nyfpmat450.
KW F1 antigen; plasmid; vaccine; plague; ds.
OS Yersinia pestis.
FH Key Location/Qualifiers
FT CDS 1..450
FT /tag= a
PN MO9824912-A2.
PD 11-JUN-1998.
PE 04-DEC-1997; 022617.
PR 04-DEC-1996; US-767115.
PA (HESK-) HESKA CORP.
PI Haanes EJ, Osorio JE, Thomas RE;
DR WPI: 98-33331/29.
PT Protection of animals against plague - using nucleic acid encoding
PT antigen from Yersinia, Pasteurella and Francisella spp.
PS Claim 8; Page 61; 75pp; English.
CC This is the nucleotide sequence of a Yersinia pestis F1 antigen, used
CC in the method of the invention. Plasmid and host cells are used to
CC produce recombinant antigens, especially Yersinia pestis antigens.
CC The recombinant antigens can be used in vaccines that are capable of
CC protecting an animal from contracting plague.
SQ Sequence 450 BP; 134 A; 102 C; 96 G; 118 T;

alignment_scores:
Quality: 634.00 Length: 149
Ratio: 4.255 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-699-716A-2 x V41601 (1)
Align seg 1/1 to: V41601 from: 1 to: 450

```
45 ADLTAATATATVEPARITLYKEGAPITIMDNGNIDTELVGTLTGG 94
|||||
2 ADLTAATATATVEPARITLYKEGAPITIMDNGNIDTELVGTLTGG 51
95 YKGTGTSTSVNFTDAAGDPMYLFTTSODGNNHOTTYVIGKDSRDEISP 144
|||||
52 YKGTGTSTSVNFTDAAGDPMYLFTTSODGNNHOTTYVIGKDSRDEISP 101
145 KVNGENLVGDVVLATGSQDFEVRISIGSKGKLAAGKYTDAVTVTVSNQ 193
|||||
102 KVNGENLVGDVVLATGSQDFEVRISIGSKGKLAAGKYTDAVTVTVSNQ 150
```

seq_name: N_Geneseq_36:V41600

seq_documentation_block:

ID V41600 standard; DNA: 474 BP.
AC V41600;
DT 26-OCT-1998 (first entry)
DE Nucleotide sequence of F1 antigen nyfpmat474.
KW F1 antigen; plasmid; vaccine; plague; ds.
OS Yersinia pestis.
FH Key Location/Qualifiers
FT CDS 7..459
FT /tag= a

FT /product= "F1 antigen"
PN W09824912-A2.
PD 11-JUN-1998.
PF 04-DEC-1997: U22617.
PR 04-DEC-1996: US-767115.
PA (HESK-) HESKA CORP
PI Hanes EJ, Osorio JE, Thomas RE;
DR WPI; 98-33331/29.
DR P-PSDB; W59787.
PT Protection of animals against plague - using nucleic acid encoding
PT antigen from Yersinia, Pasteurella and Francisella spp.
CC Claim 8, Pages 59-60; 75pp; English.
CC This is the nucleotide sequence of a Yersinia pestis F1 antigen, used
CC in the method of the invention. Plasmid and host cells are used to
CC produce recombinant antigens, especially Yersinia pestis antigens.
CC The recombinant antigens can be used in vaccines that are capable of
CC protecting an animal from contracting plague.
SQ Sequence 474 BP; 143 A; 106 C; 99 G; 126 T;

alignment_scores:
Quality: 634.00 Length: 149
Ratio: 4.255 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-699-716A-2 x V41600 (1) ..

Align seg 1/1 to: V41600 from: 1 to: 474

45 ADLTAATATATLVEPARITLTYKGGAPITIMDNGNIDTELLVGTLLT 94
|||||
4 ADLTAATATATLVEPARITLTYKGGAPITIMDNGNIDTELLVGTLLTGG 53
|||||
95 YKTGTSTSVNFTDAAGDPMYLFTSODGNHOFKTKVIGKSDRPDI 144
|||||
54 YKTGTSTSVNFTDAAGDPMYLFTSODGNHOFKTKVIGKSDRPDI 103
|||||
145 KVGNGENVGDDVVLATGSDGFVRSIGSGKGLAAGKYTDAVTVYSN 193
|||||
104 KVGNGENVGDDVVLATGSDGFVRSIGSGKGLAAGKYTDAVTVYSN 152
|||||

seq_name: N_Geneseq_36:Q92817

seq_documentation_block:
ID Q92817 standard: DNA; 541 BP.
AC Q92817;
DT 17-DEC-1995 (first entry)
DE Yersinia pestis cati (F1) antigen in plasmid pFGAL2a.
KW vaccine; antigen; Salmonella typhimurium; Salmonella typhi;
KW bubonic plague; pneumonic plague; ds.
OS Yersinia pestis.
FH Key
FT cds 2..454 location/Qualifiers
FT /*tag= a
FT misc_feature 1..6
FT /*tag= b
FT /*note= "lacZ promoter fusion site"
FT misc_feature 536..541
FT /*tag= c
FT /*note= "vector pFGAL2a bases"
PN W09518231-A1.
PD 06-JUL-1995.
PF 23-DEC-1994: G02818.
PR 24-DEC-1993: GB-026425.
PA (MINA) UK SEC FOR DEFENCE.
PI Howells A, Leaty SEC, Oyston PCF, Tlball RW, Williamson ED;
DR WPI; 95-246396/32.
DR P-PSDB; R76526.
PT DNA constructs capable of transforming microorganisms - which can be
PT used as live or attenuated vaccines which induce an immune response,
PT against Yersinia pestis, at mucosal surfaces.
PS Claim 7; Page 15-16; 27pp; English.

CC The sequence represents the plasmid pFGAL2a construct showing the
CC fusion of the first few bases of beta-galactosidase in the vector
CC with the Y. pestis cati (F1) antigen minus its signal sequence and
CC having a 5' tail including a SacI restriction site, and up to the
CC cati AAC-3' end with some vector bases. The DNA construct can be
CC used to transform human or animal gut colonizing microorganisms,
CC specifically attenuated Salmonella typhimurium or Salmonella typhi.
CC The transformed microorganisms can be used as live/attenuated
CC vaccines which induce immune responses at mucosal surfaces. The
CC vaccines provide protection against infection with Y. pestis, and
CC are parenterally and orally active vaccines offering protection
CC against bubonic and pneumonic plague.
SQ Sequence 541 BP; 163 A; 120 C; 111 G; 147 T;

alignment_scores:
Quality: 632.00 Length: 151
Ratio: 4.185 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.013

alignment_block:
US-08-699-716A-2 x Q92817 (2) ..

Align seg 1/1 to: Q92817 from: 1 to: 541

43 NADLTAATATATLVEPARITLTYKGGAPITIMDNGNIDTELLVGTLLT 92
:::|||||
1 SSADLTAATATATLVEPARITLTYKGGAPITIMDNGNIDTELLVGTLLT 50
|||||
93 GGYKGTSTSVNFTDAAGDPMYLFTSODGNHOFKTKVIGKSDRPDI 142
|||||
51 GGYKGTSTSVNFTDAAGDPMYLFTSODGNHOFKTKVIGKSDRPDI 100
|||||
143 SPKVGNGENVGDDVVLATGSDGFVRSIGSGKGLAAGKYTDAVTVYSN 192
|||||
101 SPKVGNGENVGDDVVLATGSDGFVRSIGSGKGLAAGKYTDAVTVYSN 150
|||||
193 Q 193
|
151 Q 151